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## OM protein - protein search, using sw model

Run on: June 17, 2004, 11:41:01 ; Search time 70 Seconds

(without alignments)  
456.112 Million cell updates/sec

Title: US-09-441-242a-2

Perfect score: 612  
Sequence: 1 AECPTIGRAVTHDHPRLMAW.....VYHKIDGVEDMLLELPDD 113

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*

1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	612	100.0	113	2	AAR94974 Human TCL
2	612	100.0	114	4	AAM80303 Human hae
3	612	100.0	114	4	AAM39823 Human pol
4	612	100.0	114	5	ABG95020 Human tra
5	612	100.0	114	5	ABG95021 Human tra
6	612	100.0	129	4	AAM41609 Human pol
7	573	93.6	113	2	AAR94975 Human TCL
8	318	52.0	76	4	AAM81164 Human hae
9	221	36.1	108	2	AAR94976 Mature T-
10	149	24.3	128	3	AAB18763 Amino aci
11	92	15.0	621	6	ABU28091 Protein e
12	91.5	15.0	625	6	ABU40542 Protein e
13	86	14.1	618	6	ABU47482 Protein e
14	86	14.1	619	6	ABU45553 Protein e
15	83	13.6	621	6	ABU15211 Protein e
16	83	13.6	621	6	ABU32391 Protein e
17	81	13.2	313	7	ADC23769 Protein s
18	80	13.1	251	4	ABG13152 Novel hum
19	75	12.3	275	6	ABU27326 Protein e
20	74	12.1	363	3	AAB19416 A prenyl
21	74	12.1	363	3	ABB81714 Synchocy
22	74	12.1	363	5	AAU72784 Synchocy
23	73.5	12.0	802	6	AAO26991 Pseudomon
24	73.5	12.0	802	7	ADE12165 Pseudomon
25	73.5	12.0	870	6	AAO26990 Pseudomon

26	73.5	12.0	870	7	ADE12164 Pseudomon
27	73.5	12.0	874	6	AAO26989 Pseudomon
28	73.5	12.0	874	7	ADE12163 Pseudomon
29	73.5	12.0	887	6	AAO26988 Pseudomon
30	73.5	12.0	887	7	ADE12162 Pseudomon
31	73.5	12.0	900	6	AAO26987 Pseudomon
32	73.5	12.0	900	7	ADE12161 Pseudomon
33	73.5	12.0	906	6	AAO26986 Pseudomon
34	73.5	12.0	906	7	ADE12160 Pseudomon
35	73.5	12.0	931	6	AAO26985 Pseudomon
36	73.5	12.0	931	7	ADE12159 Pseudomon
37	71.5	11.7	810	4	ABG14178 Novel hum
38	70	11.4	221	5	ABG93293 C. albica
39	70	11.4	460	6	ABP70976 Epoxide h
40	69.5	11.4	115	4	ABB60092 Human tra
41	69.5	11.4	115	4	AAH94124 Human pro
42	69	11.3	520	5	ABP60956 Mus muscu
43	69	11.3	524	5	ABP60954 Mus muscu
44	69	11.3	528	5	ABP60955 Mus muscu
45	69	11.3	2944	6	ABU56436 Lung canc

## ALIGNMENTS

RESULT 1  
AAR94974 ID AAR94974 standard; protein; 113 AA.

AC AAR94974;

DT 23-AUG-1996 (first entry)

DE Human TCL-1 polypeptide.

KW TCL-1; chromosome-14; leukemia; lymphoma; therapy; diagnosis.

OS Homo sapiens.

FX Key Location/Qualifiers

FT Modified-site 5 /label= Phosphorylation site

FT /note= "casein kinase II phosphorylation site"

XX W09613514-Al.

XX 09-MAY-1996.

XX 23-OCT-1995; 95WO-US013663.

XX 27-OCT-1994; 94US-00330272.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX (RAGG-) RAGGIO-ITALGENE SPA.

XX Russo G, Croce CM;

XX WPI; 1996-239444/24.

XX N-PSDB; AAT18876.

XX Claim 6; Page 68; 105pp; English.

The amino acid sequence of human TCL-1 protein (AAR94974) was deduced from a cDNA clone (AAT18876) obt'd. from an ALL cell line cDNA library. Recombinant TCL-1 can be obt'd. by incorporation of the cDNA into a vector and expression in Escherichia coli transformants. The TCL-1 protein and antibodies raised against it can be used for the diagnosis and treatment of conditions associated with increased expression of TCL-1 proteins and/or with chromosomal abnormalities, esp. T-cell leukemia and

CC lymphomas with chromosome 14 abnormalities  
XX  
SQ Sequence 113 AA;  
Query Match 100.0%; Score 612; DB 2; Length 113;  
Best Local Similarity 100.0%; Pred. No. 4,6e-68;  
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AECPTLGEAVTDHPRLMAMEKEFYVLDEKQHWLPLTTEIKRLOLRVLLRRDVLGRP 60  
DB 1 AECPTLGEAVTDHPRLMAMEKEFYVLDEKQHWLPLTTEIKRLOLRVLLRRDVLGRP 60  
QY 61 MTPPTQIGPSLLPIMWOLYPPDGRYRSSDSFWRLVYHIKIDGVEDMLLELLPDD 113  
DB 61 MTPPTQIGPSLLPIMWOLYPPDGRYRSSDSFWRLVYHIKIDGVEDMLLELLPDD 113  
RESULT 2  
AAM80303  
ID AAM80303 standard; protein; 114 AA.  
XX  
AC AAM80303;  
XX  
DT 13-NOV-2001 (first entry)  
XX  
DE Human haematological malignancy-related antigen #1.  
XX  
KW Human; cytostatic; vascular; gene therapy; vaccine; lymphoma;  
KW haematological malignancy; antigen; chronic lymphocytic leukaemia;  
KW follicular lymphoma; Hodgkin's lymphoma; non-Hodgkin's lymphoma.  
XX  
OS Homo sapiens.  
XX  
PN WO200164886-A2.  
XX  
PD 07-SEP-2001.  
XX  
PF 01-MAR-2001; 2001WO-US007272.  
XX  
PR 01-MAR-2000; 2000US-0186126P.  
PR 17-MAR-2000; 2000US-0190479P.  
PR 27-APR-2000; 2000US-0200545P.  
PR 28-APR-2000; 2000US-0200303P.  
PR 28-APR-2000; 2000US-0200779P.  
PR 01-MAY-2000; 2000US-020084P.  
PR 04-MAY-2000; 2000US-0206201P.  
PR 22-MAY-2000; 2000US-0218950P.  
PR 14-JUL-2000; 2000US-0222903P.  
PR 03-AUG-2000; 2000US-0223416P.  
PR 04-AUG-2000; 2000US-0223378P.  
PR 07-AUG-2000; 2000US-0223378P.  
XX  
PA (CORI-) CORIXA CORP.  
XX  
PI Gaiger A, Algate PA, Mannion J;  
XX  
DR WPI; 2001-514842/56.  
XX  
PT Compositions and methods for the detection of hematological malignancies,  
PT e.g. chronic lymphocytic leukemia, lymphoma, follicular lymphoma and  
PT Hodgkin's and T/B cell non-Hodgkin's lymphoma.  
XX  
PS Claim 31; Page 504; 1252pp; English.  
XX  
XX The present invention relates to compositions and methods for the  
CC detection, diagnosis and therapy of haematological malignancies. The  
CC present sequence is the protein sequence of a human haematological  
CC malignancy related antigen. The methods of the present invention comprise  
CC detecting the presence of haematological malignancy related antigen(s) in  
CC a sample obtained from the patient (an increased level of the  
CC polypeptide, compared to an unaffected individual, is indicative of an  
CC increased risk). Hematological malignancies which can be treated using  
CC the present invention are chronic lymphocytic leukaemia, lymphoma,

CC follicular lymphoma, Hodgkin's lymphoma, non-Hodgkin's lymphoma and T/B  
CC cell non-Hodgkin's lymphoma  
XX  
SQ Sequence 114 AA;  
Query Match 100.0%; Score 612; DB 4; Length 114;  
Best Local Similarity 100.0%; Pred. No. 4,7e-68;  
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AECPTLGEAVTDHPRLMAMEKEFYVLDEKQHWLPLTTEIKRLOLRVLLRRDVLGRP 60  
DB 2 AECPTLGEAVTDHPRLMAMEKEFYVLDEKQHWLPLTTEIKRLOLRVLLRRDVLGRP 61  
QY 61 MTPPTQIGPSLLPIMWOLYPPDGRYRSSDSFWRLVYHIKIDGVEDMLLELLPDD 113  
DB 62 MTPPTQIGPSLLPIMWOLYPPDGRYRSSDSFWRLVYHIKIDGVEDMLLELLPDD 114  
RESULT 3  
AAM39823  
ID AAM39823 standard; protein; 114 AA.  
XX  
AC AAM39823;  
XX  
DT 22-OCT-2001 (first entry)  
XX  
DE Human polypeptide SEQ ID NO 2968.  
XX  
KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;  
KW peripheral nervous system; neuropathy; central nervous system; CNS;  
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemoclastic;  
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
KW leukaemia.  
XX  
OS Homo sapiens.  
XX  
PN WO200153312-A1.  
XX  
PD 26-JUL-2001.  
XX  
PF 26-DEC-2000; 2000WO-US034263.  
XX  
PR 23-DEC-1999; 99US-00471275.  
PR 21-JAN-2000; 2000US-00498725.  
PR 25-APR-2000; 2000US-00552317.  
PR 20-JUN-2000; 2000US-00596042.  
PR 19-JUL-2000; 2000US-00620312.  
PR 03-AUG-2000; 2000US-00653450.  
PR 14-SEP-2000; 2000US-00662191.  
PR 19-OCT-2000; 2000US-00693036.  
PR 29-NOV-2000; 2000US-00727344.  
XX  
XX (HYSE-) HYSEQ INC.  
XX  
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;  
PI Zhou P, Goodrich R, Dmanac RT;  
XX  
DR WPI; 2001-442253/47.  
XX  
DR N-PSDB; AAI58979.  
XX  
PT Novel nucleic acids and polypeptides, useful for treating disorders such  
PT as central nervous system injuries.  
XX  
PS Example 4; SEQ ID NO 2968; 10078pp; English.  
XX  
XX The invention relates to human nucleic acids (AA157798-AA161369) and the  
CC encoded polypeptides (AAM36642-AA42213) with nootropic,  
CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
CC in gene therapy. A composition containing a polypeptide or polynucleotide  
CC system, such as peripheral nervous injuries, peripheral neuropathy and

CC localised neuropathies and central nervous system diseases, such as  
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
CC utilisation of the activities such as: Immune system suppression,  
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
CC assays for receptor activity, arthritis and inflammation, leukaemias and  
CC C.N.S disorders. Note: The sequence data for this patent did not form  
CC part of the printed specification

SQ Sequence 114 AA;

Query Match 100.0%; Score 612; DB 4; Length 114;  
Best Local Similarity 100.0%; Pred. No. 4,7e-68;  
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AECPTLGEAVTDHPRLWAMEKFVYLDEKQHAMLPETIEIKDRLQLRVLLRREDVVLGRP 60  
DB 2 AECPTLGEAVTDHPRLWAMEKFVYLDEKQHAMLPETIEIKDRLQLRVLLRREDVVLGRP 61  
QY 61 MPTPTIGPSLLPIMMQLYPDGRYRSSDSSFMRLLVYHIKIDGVEDMLLELPDD 113  
DB 62 MPTPTIGPSLLPIMMQLYPDGRYRSSDSSFMRLLVYHIKIDGVEDMLLELPDD 114

## RESULT 4

ABG95020

ID ABG95020 standard; protein; 114 AA.

AC ABG95020;

DT 04-DEC-2002 (first entry)

DE Human translocation inv14(q11, q32) protein #1.

KM Chromosome aberration; oncogenic fusion protein; cancer;  
KM proliferative disease; cellular protein isoform; heat shock protein 90;  
KM HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;  
KM T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;  
KM acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;  
KM acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;  
KM papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;  
KM rhabdomyosarcoma; synovial sarcoma; viral infection.

OS Homo sapiens.

PN WO200269900-A2.

PD 12-SEP-2002.

PP 01-MAR-2002; 2002WO-US006518.

PR 01-MAR-2001; 2001US-0272751P.

PA (CONF-) CONFORMA THERAPEUTICS CORP.

PI Fritz LC, Burrows FJ;

PR WPI; 2002-698710/75.

DR N-PSDB; ABS73183.

PT Treating genetically-defined disease associated with chromosomal  
PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative  
PT diseases, involves administering an inhibitor of heat shock protein 90.

PS Disclosure; Page 103; 389pp; English.

CC The invention describes a method of treating genetically-defined disease  
CC associated with chromosomal aberrations yielding oncogenic fusion  
CC proteins (I), treating cancerous cells containing (I) in a heterogeneous  
CC cell population, treating proliferative diseases associated with mutant  
CC protein or cellular protein isoforms (II), dependent on heat shock protein  
CC (HSP)-90, or selectively treating cells expressing (II) involving

CC administering HSP90-inhibitor. The method is useful for treating  
CC genetically-defined disease with chromosomal aberration yielding  
CC oncogenic fusion protein, treating cancerous cells containing fusion  
CC protein in heterogeneous cell population, treating proliferative disease  
CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or  
CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.  
CC p53), or selectively treating cells expressing mutant protein or cellular  
CC protein isoform in a patient heterozygous for (II). The method is useful  
CC for treating a disease e.g. haematopoietic disorder such as T or B cell  
CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CMML,  
CC or a disease characterised by a solid tumour such as papillary thyroid  
CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and  
CC synovial sarcoma. The method is also useful for treating viral  
CC infections. This represents a protein encoded by the DNA sequence of a  
CC chromosome aberration

SQ Sequence 114 AA;

Query Match 100.0%; Score 612; DB 5; Length 114;  
Best Local Similarity 100.0%; Pred. No. 4,7e-68;  
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AECPTLGEAVTDHPRLWAMEKFVYLDEKQHAMLPETIEIKDRLQLRVLLRREDVVLGRP 60  
DB 2 AECPTLGEAVTDHPRLWAMEKFVYLDEKQHAMLPETIEIKDRLQLRVLLRREDVVLGRP 61  
QY 61 MPTPTIGPSLLPIMMQLYPDGRYRSSDSSFMRLLVYHIKIDGVEDMLLELPDD 113  
DB 62 MPTPTIGPSLLPIMMQLYPDGRYRSSDSSFMRLLVYHIKIDGVEDMLLELPDD 114

## RESULT 5

ABG95021

ID ABG95021 standard; protein; 114 AA.

AC ABG95021;

DT 04-DEC-2002 (first entry)

DE Human translocation inv14(q11, q32) protein #2.

KM Chromosome aberration; oncogenic fusion protein; cancer;  
KM proliferative disease; cellular protein isoform; heat shock protein 90;  
KM HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;  
KM T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;  
KM acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;  
KM acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;  
KM papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;  
KM rhabdomyosarcoma; synovial sarcoma; viral infection.

OS Homo sapiens.

PN WO200269900-A2.

PD 12-SEP-2002.

PP 01-MAR-2002; 2002WO-US006518.

PR 01-MAR-2001; 2001US-0272751P.

PA (CONF-) CONFORMA THERAPEUTICS CORP.

PI Fritz LC, Burrows FJ;

PR WPI; 2002-698710/75.

DR N-PSDB; ABS73184.

PT Treating genetically-defined disease associated with chromosomal  
PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative  
PT diseases, involves administering an inhibitor of heat shock protein 90.

PS Disclosure; Page 104; 389pp; English.

CC The invention describes a method of treating genetically-defined disease  
 CC associated with chromosomal aberrations yielding oncogenic fusion  
 CC proteins (I); treating cancerous cells containing (I) in a heterogeneous  
 CC cell population; treating proliferative diseases associated with mutant  
 CC protein or cellular protein isoforms (II) dependent on heat shock protein  
 CC (HSP)-90, or selectively treating cells expressing (II) involving  
 CC administering HSP90-inhibitor. The method is useful for treating  
 CC genetically-defined disease with chromosomal aberration yielding  
 CC oncogenic fusion protein, treating cancerous cells containing fusion  
 CC protein in heterogeneous cell population, treating proliferative disease  
 CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or  
 CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.  
 CC p53), or selectively treating cells expressing mutant protein or cellular  
 CC protein isoform in a patient heterozygous for (II). The method is useful  
 CC for treating a disease e.g. haematopoietic disorder such as T or B cell  
 CC lymphoma, chronic myeloid leukemia (CML), APL, ALL, AML, NHL and CML,  
 CC or a disease characterised by a solid tumour such as papillary thyroid  
 CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and  
 CC synovial sarcoma. The method is also useful for treating viral  
 CC infections. This represents a protein encoded by the DNA sequence of a  
 CC chromosome aberration

CC Sequence 114 AA;

Query Match 100.0%; Score 612; DB 5; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-68;  
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AECPTLGEAVTDHPRLMAWEKFFVYLDEKQAMLPITIEIKDRLQRLVLRREDVVLGRP 60

DB 2 AECPTLGEAVTDHPRLMAWEKFFVYLDEKQAMLPITIEIKDRLQRLVLRREDVVLGRP 61

QY 61 MTPFOIGPSLLPIMQOLYPDGRYSSDSFWRVLVYHIKIDGVEDMLLELPDD 113

DB 62 MTPFOIGPSLLPIMQOLYPDGRYSSDSFWRVLVYHIKIDGVEDMLLELPDD 114

RESULT 6  
 AAM41609  
 ID AAM41609 standard; protein; 129 AA.

AC AAM41609;

DT 22-OCT-2001 (first entry)

XX Human polypeptide SEQ ID NO 6540.

XX Human, nootropic; immunosuppressant; cyostatic; gene therapy; cancer;  
 XX peripheral nervous system; neuropathy; central nervous system; CNS;  
 XX Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
 XX amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
 XX chemoknetic; thrombolytic; drug screening; arthritis; inflammation;  
 XX leukaemia.

XX Homo sapiens.

OS WO200153312-A1.

XX 26-JUL-2001.

PF 26-DEC-2000; 2000WO-US034263.

XX 23-DEC-1999; 99US-00471275.

PR 21-JAN-2000; 2000US-0048725.

PR 25-APR-2000; 2000US-00552317.

PR 20-JUN-2000; 2000US-00598042.

PR 19-JUL-2000; 2000US-00620312.

PR 03-AUG-2000; 2000US-00653450.

PR 14-SEP-2000; 2000US-00662191.

PR 19-OCT-2000; 2000US-00693036.

PR 29-NOV-2000; 2000US-00727344.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Aundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D,  
 PI Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA,  
 PI Zhou P, Goodrich R, Drmanac RT;  
 XX WPI; 2001-442253/47.  
 DR N-PSDB; AAI60765.

PT Novel nucleic acids and polypeptides, useful for treating disorders such  
 PT as central nervous system injuries.

XX Example 2; SEQ ID NO 6540; 10078pp; English.

CC The invention relates to human nucleic acids (AA157798-AA161369) and the  
 CC encoded polypeptides (AAM38642-AA42213) with nootropic,  
 CC immunosuppressant and cyostatic activity. The polynucleotides are useful  
 CC in gene therapy. A composition containing a polypeptide or polynucleotide  
 CC of the invention may be used to treat diseases of the peripheral nervous  
 CC system, such as peripheral nervous injuries, peripheral neuropathy and  
 CC localised neuropathies and central nervous system diseases, such as  
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
 CC utilisation of the activities such as: Immune system suppression,  
 CC Activin/inhibin activity, chemotactic/chemoknetic activity, haemostatic  
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
 CC assays for receptor activity, arthritis and inflammation, leukaemia and  
 CC C.N.S disorders. Note: The sequence data for this patent did not form  
 CC part of the printed specification

XX Sequence 129 AA;

Query Match 100.0%; Score 612; DB 4; Length 129;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-68;  
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AECPTLGEAVTDHPRLMAWEKFFVYLDEKQAMLPITIEIKDRLQRLVLRREDVVLGRP 60

DB 17 AECPTLGEAVTDHPRLMAWEKFFVYLDEKQAMLPITIEIKDRLQRLVLRREDVVLGRP 76

QY 61 MTPFOIGPSLLPIMQOLYPDGRYSSDSFWRVLVYHIKIDGVEDMLLELPDD 113

DB 77 MTPFOIGPSLLPIMQOLYPDGRYSSDSFWRVLVYHIKIDGVEDMLLELPDD 129

RESULT 7

ID AAR94975 standard; protein; 113 AA.

AC AAR94975;

DT 23-AUG-1996 (first entry)

XX Human TCL-1 polypeptide.

XX TCL-1; chromosome-14; leukaemia; lymphoma; therapy.

XX Homo sapiens.

OS Location/Qualifiers

FH Key 31 /note= "unidentified amino acid"

FT MISC-difference 46 /note= "unidentified amino acid"

FT MISC-difference 47 /note= "unidentified amino acid"

FT MISC-difference 55 /note= "unidentified amino acid"

XX WO9613514-A1.

XX 09-MAY-1996.

PF 23-OCT-1995; 95WO-US013663.

XX 27-OCT-1994; 94US-00330272.  
 PR (UYJE-) UNIV JEFFERSON THOMAS.  
 PA (RAGG-) RAGGIO-ITALGENE SPA.  
 XX  
 PI Russo G, Croce CM;  
 XX  
 DR MPI: 1996-239444/24.  
 DR N-PSDB; AAT18877.  
 XX  
 PT New TCR-1 protein and gene associated with chromosome 14 abnormalities -  
 PT useful to develop prods. for detection, treatment and prevention of  
 PT diseases such as T-cell leukaemia(s) and lymphoma(s).  
 XX  
 PS Disclosure; Page 69-72; 105pp; English.  
 XX  
 CC The amino acid sequence (AAR94975) of human TCR-1 protein was deduced  
 CC from the exon sequences of the TCR-1 gene (AAT18877). A sequence deduced  
 CC from a cDNA clone is given in AAR94974. The TCR-1 gene is expressed at  
 CC high levels in leukaemic cells carrying a t(14;14)(q11;q32) translocation  
 CC or an inv(14)(q11;q32) inversion. The TCR-1 protein, and antibodies  
 CC raised against it, can be used for the diagnosis or treatment of  
 CC conditions associated with increased expression of TCR-1 proteins and/or  
 CC with chromosome 14 abnormalities, esp. T-cell leukaemia and lymphoma  
 XX  
 SQ Sequence 113 AA;

Query Match 93.6%; Score 573; DB 2; Length 113;  
 Best Local Similarity 95.6%; Pred. No. 3.4e-63;  
 Matches 108; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 AECPTLGEAVTDHPRLMAWEKRYVLDKQHAWLPITTEIKRQLRLVLRREDVVLGR 60  
 DB 1 AECPTLGEAVTDHPRLMAWEKRYVLDKQKXCLPITTEIKRQLRXVLRREDVVLGR 60  
 QY 61 MPTPIGSLPLIMQVLYPDGRYRSSDSFMRVLYVHIKIDGVEDMLLELPDD 113  
 DB 61 MPTPIGSLPLIMQVLYPDGRYRSSDSFMRVLYVHIKIDGVEDMLLELPDD 113

RESULT 8  
 AAM81164  
 ID AAM81164 standard; protein; 76 AA.  
 XX  
 AC AAM81164;  
 XX  
 DT 13-NOV-2001 (first entry)  
 DE Human haematological malignancy-related antigen #862.  
 XX  
 KM Human; cytostatic; vascular; gene therapy; vaccine; lymphoma;  
 KM haematological malignancy; antigen; chronic lymphocytic leukaemia;  
 KM follicular lymphoma; Hodgkin's lymphoma; non-Hodgkin's lymphoma.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO200164886-A2.  
 XX  
 PD 07-SEP-2001.  
 XX  
 PF 01-MAR-2001; 2001WO-US007272.  
 XX  
 PR 01-MAR-2000; 2000US-0186126P.  
 PR 17-MAR-2000; 2000US-0190479P.  
 PR 27-APR-2000; 2000US-0200545P.  
 PR 28-APR-2000; 2000US-0200303P.  
 PR 28-APR-2000; 2000US-0200779P.  
 PR 01-MAY-2000; 2000US-0200999P.  
 PR 04-MAY-2000; 2000US-0202084P.  
 PR 22-MAY-2000; 2000US-0206201P.  
 PR 14-JUL-2000; 2000US-0218950P.  
 PR 03-AUG-2000; 2000US-0222903P.

PR 04-AUG-2000; 2000US-0223416P.  
 PR 07-AUG-2000; 2000US-0223378P.  
 XX  
 PA (CORI-) CORIXA CORP.  
 XX  
 PI Galger A, Algate PA, Mannion J;  
 XX  
 DR MPI: 2001-514842/56.  
 XX  
 PT Compositions and methods for the detection of hematological malignancies,  
 PT e.g. chronic lymphocytic leukemia, lymphoma, follicular lymphoma and  
 PT Hodgkin's and T/B cell non-Hodgkin's lymphoma.  
 XX  
 PS Claim 1; Page 859; 1252pp; English.

CC The present invention relates to compositions and methods for the  
 CC detection, diagnosis and therapy of haematological malignancies. The  
 CC present sequence is the protein sequence of a human haematological  
 CC malignancy related antigen. The methods of the present invention comprise  
 CC detecting the presence of haematological malignancy related antigen(s) in  
 CC a sample obtained from the patient (an increased level of the  
 CC polypeptide, compared to an unaffected individual, is indicative of an  
 CC increased risk). Haematological malignancies which can be treated using  
 CC the present invention are chronic lymphocytic leukaemia, lymphoma,  
 CC follicular lymphoma, Hodgkin's lymphoma, non-Hodgkin's lymphoma and T/B  
 CC cell non-Hodgkin's lymphoma  
 XX  
 SQ Sequence 76 AA;

Query Match 52.0%; Score 318; DB 4; Length 76;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-31;  
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AECPTLGEAVTDHPRLMAWEKRYVLDKQHAWLPITTEIKRQLRLVLRREDVVLGR 59  
 DB 18 AECPTLGEAVTDHPRLMAWEKRYVLDKQHAWLPITTEIKRQLRLVLRREDVVLGR 76

RESULT 9  
 AAR94976  
 ID AAR94976 standard; protein; 108 AA.  
 XX  
 AC AAR94976;  
 XX  
 DT 23-AUG-1996 (first entry)  
 DE Mature T-cell proliferative 1 protein.  
 XX  
 KM TCR-1; chromosome-14; leukaemia; lymphoma; therapy; diagnosis;  
 KM T-cell proliferative 1 protein.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 108  
 FT /note= "unidentified amino acid"  
 XX  
 FN WO9613514-A1.  
 XX  
 PD 09-MAY-1996.  
 XX  
 PF 23-OCT-1995; 95WO-US013663.  
 XX  
 PR 27-OCT-1994; 94US-00330272.  
 XX  
 PA (UYJE-) UNIV JEFFERSON THOMAS.  
 PA (RAGG-) RAGGIO-ITALGENE SPA.  
 XX  
 PI Russo G, Croce CM;  
 XX  
 DR MPI: 1996-239444/24.  
 XX  
 PT New TCR-1 protein and gene associated with chromosome 14 abnormalities -

PT useful to develop prods. for detection, treatment and prevention of  
PT diseases such as T-cell leukaemia(s) and lymphoma(s).  
XX  
PS Disclosure; Page 69; 105pp; English.  
XX  
CC The mature T-cell proliferative 1 protein (AAR94976) is involved in a  
CC translocation of chromosome 14 and X chromosome t(14;X)(q11;q28). It  
CC shows 40% amino acid sequence homology to human Tc1-1 protein (AAR94974),  
CC which is associated with chromosome 14 abnormalities leading to leukaemia  
CC and lymphoma  
XX  
SQ Sequence 108 AA;  
Query Match 36.1%; Score 221; DB 2; Length 108;  
Best Local Similarity 40.2%; Pred. No. 2.4e-19;  
Matches 43; Conservative 23; Mismatches 39; Indels 2; Gaps 1;  
QY 7 GEAVTDHEDRLAMEKFPVYLDEKQHWMLPLTIEIKDRLQLRREDVVLGRPTPTQI 66  
DB 3 GEDVGAPDPDHLMWQEGYRDEYQRTWVAVVEEESFLARAV--QGIQVPLGDARPSHL 60  
QY 67 GPSLLPTMWQLYPDGRYSSDSFWRVLYHIKIDGVEDMLLELPD 113  
DB 61 LTSQPLPMWQLYPERRYMNNRSLMOIOHMLVWGVGVELIKLPLPD 107  
RESULT 10  
AAB18763  
ID AAB18763 standard; protein; 128 AA.  
XX  
AC AAB18763;  
XX  
DT 22-JAN-2001 (first entry)  
XX  
DE Amino acid sequence of the human Tc1-1b protein.  
XX  
XX Tc1-1; Tc1-1b; T cell malignancy; chromosome 14 abnormality; lymphoma;  
KM T-cell leukaemia; immunodeficiency syndrome; ataxia-telangiectasia.  
XX  
OS Homo sapiens.  
XX  
PN W020055169-A1.  
XX  
PD 21-SEP-2000.  
XX  
PF 15-MAR-2000; 2000WO-US006612.  
XX  
PR 15-MAR-1999; 99US-0124714P.  
XX  
PA (UYJE-) UNIV JEFFERSON THOMAS.  
XX  
PI Croce CM, Pekarsky Y;  
XX  
DR WPI; 2000-611514/58.  
DR N-PSDB; AAA75822.  
XX  
PT Novel nucleic acid of Tc1-1 gene family, Tc1-1b, expressed in low levels  
PT in normal bone marrow and peripheral lymphocytes, but activated in T-cell  
PT leukemia and lymphoma, used to identify chromosome 14 abnormalities.  
XX  
PS Claim 7; Page 64; 70pp; English.  
XX  
CC The present sequence represents a human Tc1-1b protein. The Tc1-1b gene  
CC is implicated in the development of T cell malignancies. Fragments of Tc1  
CC -1b cDNA sequences are used for detecting a target sequence indicating a  
CC chromosome 14 abnormality, such as a (14;14)(q11;q32) translocation or a  
CC (14)(q11;q32) inversion. Tc1-1b antisense sequences and antibodies are  
CC useful for treating a disease state such as T-cell leukemia or lymphoma  
CC associated with a chromosome 14 abnormality. The Tc1-1b gene and its gene  
CC product are useful for treating disease states associated with the Tc1-1b  
CC locus on chromosome protein including T-prolymphocytic leukaemias, acute  
CC and chronic leukaemias associated with the immunodeficiency syndrome  
CC ataxia-telangiectasia (AT)

XX  
SQ Sequence 128 AA;  
Query Match 24.3%; Score 149; DB 3; Length 128;  
Best Local Similarity 29.2%; Pred. No. 2.8e-10;  
Matches 33; Conservative 21; Mismatches 45; Indels 14; Gaps 1;  
QY 14 PDRLMAWEKFPVYLDEKQHWMLPLTIEIKDRLQ-----LRVLLREDVVLGR 59  
DB 13 PGRIMIGRPGIYEDDEERTWTVVVRNPSRRKEMARASQGSRYEPSTIVLMQMAVHTRE 72  
QY 60 PMPTQIGPSLLPTMWQLYPDGRYSSDSFWRVLYHIKIDGVEDMLLELPD 112  
DB 73 LLSGQWPFQPLPAVWQLYGGRKYRADSSFWELIADHGQIDSEQVLTGYQPE 125  
RESULT 11  
AABU28091  
ID AABU28091 standard; protein; 621 AA.  
XX  
AC AABU28091;  
XX  
DT 19-JUN-2003 (first entry)  
XX  
DE Protein encoded by Prokaryotic essential gene #13618.  
XX  
XX Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX  
OS Enterobacter cloacae.  
XX  
PN W020027183-A2.  
XX  
PD 03-OCT-2002.  
XX  
PF 21-MAR-2002; 2002WO-US009107.  
XX  
PR 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX  
PA (ELIT-) ELITRA PHARM INC.  
XX  
PI Wang L, Zamudio C, Malone C, Haeselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick UD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX  
DR WPI; 2003-023926/02.  
DR N-PSDB; ACA31961.  
XX  
PT New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX  
PS Claim 25; SEQ ID NO 56015; 1766pp; English.  
XX  
CC The invention relates to an isolated nucleic acid comprising any one of  
CC the 613 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a

CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
CC  
XX  
SQ Sequence 621 AA;  
  
Query Match 15.0%; Score 92; DB 6; Length 621;  
Best Local Similarity 33.3%; Pred. No. 0.026;  
Matches 25; Conservative 16; Mismatches 26; Indels 8; Gaps 3;  
  
QY 16 RLMAWEKRV---YLDKQAMLPRTI---EIKDRLQLRLRLREDVVLGRMPTQTGP 68  
DB 440 KTWAMETALIQIREVSETEYAAVPIRTGHPGEVRL-IDVLRPEVLVFEPLMTVIPIGNK 498  
QY 69 SLPLPMQVLPDGRY 83  
DB 499 AILPVLMQVFPVHRY 513  
  
RESULT 12  
ABU40542  
ID ABU40542 standard; protein; 625 AA.  
XX  
AC ABU40542;  
XX  
DT 19-JUN-2003 (first entry)  
XX  
DE Protein encoded by Prokaryotic essential gene #26069.  
XX  
KM Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX  
OS Proteus sp.  
XX  
PN WO200277183-A2.  
XX  
PD 03-OCT-2002.  
XX  
PF 21-MAR-2002; 2002WO-US009107.  
XX  
PR 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX  
XX (ELIT-) ELITRA PHARM INC.  
XX  
F1 Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
F1 Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX  
DR WPI; 2003-029926/02.  
DR N-PDB; ACA44412.  
XX  
XX New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX  
XX Claim 25; SEQ ID NO 68466; 1766pp; English.  
XX  
CC The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:

CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a gene that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
CC  
XX  
SQ Sequence 625 AA;  
  
Query Match 15.0%; Score 91.5; DB 6; Length 625;  
Best Local Similarity 33.3%; Pred. No. 0.03;  
Matches 26; Conservative 13; Mismatches 24; Indels 15; Gaps 4;  
  
QY 16 RLMAWEKRVYLDK---KQAMLPRTI---EIKDRLQLRLRLREDVVLGRMPTQTGP 65  
DB 441 KTWAME--TALDQRESEQSLPIRTGDPAGEVR--LVDVLRPEVITVFEPLMTILP 495  
QY 66 IGPLPLPMQVLPDGRY 83  
DB 496 SNKAILPLTMQLFPDNPY 513  
  
RESULT 13  
ABU47482  
ID ABU47482 standard; protein; 618 AA.  
XX  
AC ABU47482;  
XX  
DT 19-JUN-2003 (first entry)  
XX  
DE Protein encoded by Prokaryotic essential gene #33009.  
XX  
KM Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX  
OS Salmomella typhi.  
XX  
PN WO200277183-A2.  
XX  
PD 03-OCT-2002.  
XX  
PF 21-MAR-2002; 2002WO-US009107.  
XX  
PR 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX  
XX (ELIT-) ELITRA PHARM INC.  
XX  
F1 Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
XX  
PI





ABU15211  
ID ABU15211 standard; protein; 619 AA.  
XX AC ABU15211;  
XX DT 19-JUN-2003 (first entry)  
XX DE Protein encoded by Prokaryotic essential gene #738.  
KM Antisense; prokaryotic essential gene; cell proliferation; drug design.  
OS Escherichia coli.  
XX MO000277183-A2.  
PD 03-OCT-2002.  
XX 21-MAR-2002; 2002MO-US009107.  
PF 21-MAR-2001; 2001US-00815243.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342823P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
PA (ELIT-) ELITRA PHARM INC.  
XX Wang L, Zamudio C, Malone C, Haseelbeck R, Ohlsen KL, Zyskind JW,  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX WPI; 2003-029926/02.  
DR N-PSDB; ACA19081.  
PT New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.

Claim 25; SEQ ID NO 4135; 1766bp; English.

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:  
(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-regulated gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

Sequence 619 AA;

Query	March	13.6%	Score 83;	DB 6;	Length 619;
Best Local Similarity	28.4%;	Pred. No. 0.34;			
Matches	21;	Conservative	21;	Mismatches	26;
				Indels	6;
				Gaps	3
Oy	16	RUMAME----	KFYVLDEKOHAMLP-	TEIHDRLOLRVLREDVVLGPM-	TPNQIGPS 69
		: : :	: : :	: : :	: : :
		: : :	: : :	: : :	: : :
Db	440	KTMAMEFADIREVSDREFAAFVPIRTGHPQNEVALIDVL	LRPEVLFEPLMTVIPGNKA		499
Oy	70	LLPIIMOLYPPGRY	83		
		: : :	: : :		
Db	500	ILPIIMSLFPHHRY	513		

Search completed: June 17, 2004, 14:26:21  
Job time : 72 secs

Sequence 619 AA;

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 17, 2004, 14:26:27 ; Search time 503 Seconds  
(without alignments)  
63.422 Million cell updates/sec

Title: US-09-441-242a-2

Perfect score: 612  
Sequence: 1 AECPTLGEAVTDHPRLMW.....VYHIKIDGVEDMLLELLPDD 113

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 1163542 seqs, 282313646 residues

Total number of hits satisfying chosen parameters: 1163542

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications\_AA:\*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
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18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	612	100.0	114	9	US-09-796-692-666
2	612	100.0	114	14	US-10-040-862-666
3	612	100.0	114	15	US-10-057-475B-666
4	612	100.0	114	15	US-10-154-884B-666
5	612	100.0	121	15	US-10-057-475B-10485
6	612	100.0	121	15	US-10-154-884B-10485
7	318	52.0	76	9	US-09-796-692-1528
8	318	52.0	76	14	US-10-040-862-1528
9	318	52.0	76	15	US-10-057-475B-1528
10	318	52.0	76	15	US-10-154-884B-1528
11	92	15.0	621	12	US-10-282-122A-56015
12	91.5	15.0	623	12	US-10-282-122A-56015
13	86	14.1	618	12	US-10-282-122A-68466
14	86	14.1	619	12	US-10-282-122A-75406
15	83	13.6	619	12	US-10-282-122A-43135

16	83	13.6	621	12	US-10-282-122A-60315	Sequence 60315, A
17	81	13.2	313	12	US-10-440-503-36	Sequence 36, Appl
18	81	13.2	313	12	US-10-461-925-36	Sequence 36, Appl
19	81	13.2	313	14	US-10-146-772-36	Sequence 36, Appl
20	81	13.2	313	15	US-10-241-742-36	Sequence 36, Appl
21	81	13.2	313	15	US-10-440-523-36	Sequence 36, Appl
22	75	12.3	275	12	US-10-282-122A-55250	Sequence 55250, A
23	74	12.1	363	14	US-10-349-508-39	Sequence 39, Appl
24	74	12.1	363	15	US-10-437-159-39	Sequence 39, Appl
25	74	12.1	363	16	US-10-471-243-22	Sequence 22, Appl
26	70	11.4	422	14	US-10-272-490-88	Sequence 88, Appl
27	70	11.4	460	14	US-10-214-473-40	Sequence 40, Appl
28	70	11.4	460	14	US-10-272-490-40	Sequence 40, Appl
29	69	11.3	520	14	US-10-032-201B-305	Sequence 305, Appl
30	69	11.3	524	14	US-10-032-201B-303	Sequence 303, Appl
31	69	11.3	528	14	US-10-032-201B-304	Sequence 304, Appl
32	68	11.1	115	15	US-10-108-260A-3222	Sequence 3222, Ap
33	68	11.1	213	9	US-09-738-626-4741	Sequence 4741, Ap
34	68	11.1	216	9	US-09-935-757-2	Sequence 2, Appl
35	68	11.1	216	9	US-09-935-757-6	Sequence 6, Appl
36	68	11.1	1321	16	US-10-408-765A-2241	Sequence 2241, Ap
37	67	10.9	206	14	US-10-192-988-19	Sequence 19, Appl
38	67	10.9	432	14	US-10-214-473-28	Sequence 28, Appl
39	67	10.9	432	14	US-10-272-490-28	Sequence 28, Appl
40	66	10.8	196	13	US-10-081-281-109	Sequence 109, Appl
41	66	10.8	448	13	US-10-015-536-17	Sequence 17, Appl
42	66	10.8	448	13	US-10-081-281-111	Sequence 11, Appl
43	66	10.8	500	9	US-09-766-378A-25	Sequence 25, Appl
44	66	10.8	562	9	US-09-815-837-70	Sequence 70, Appl
45	66	10.8	702	12	US-10-282-122A-78032	Sequence 78032, A

#### ALIGNMENTS

RESULT 1  
US-09-796-692-666  
Sequence 666, Application US/09796692  
Publication No. US20020198362A1  
GENERAL INFORMATION:  
APPLICANT: Galger, Alexander  
APPLICANT: Mannion, Jane  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY  
FILE REFERENCE: 2077.001200  
CURRENT FILING DATE: 2001-03-01  
PRIOR APPLICATION NUMBER: US/09/796, 692  
PRIOR FILING DATE: 2000-03-01  
PRIOR APPLICATION NUMBER: 60/196, 126  
PRIOR FILING DATE: 2000-03-01  
PRIOR APPLICATION NUMBER: 60/190, 479  
PRIOR FILING DATE: 2000-03-17  
PRIOR APPLICATION NUMBER: 60/200, 545  
PRIOR FILING DATE: 2000-04-27  
PRIOR APPLICATION NUMBER: 60/200, 303  
PRIOR FILING DATE: 2000-04-28  
PRIOR APPLICATION NUMBER: 60/200, 779  
PRIOR FILING DATE: 2000-04-28  
PRIOR APPLICATION NUMBER: 60/200, 999  
PRIOR FILING DATE: 2000-05-01  
PRIOR APPLICATION NUMBER: 60/202, 084  
PRIOR FILING DATE: 2000-05-04  
PRIOR APPLICATION NUMBER: 60/206, 201  
PRIOR FILING DATE: 2000-05-22  
PRIOR APPLICATION NUMBER: 60/218, 950  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: 60/222, 903  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: 60/223, 416  
PRIOR FILING DATE: 2000-08-04  
PRIOR APPLICATION NUMBER: 60/223, 378  
PRIOR FILING DATE: 2000-08-07  
NUMBER OF SEQ ID NOS: 9597

```
SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 666
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-692-666
```

```
Query Match          100.0%; Score 612; DB 9; Length 114;
Best Local Similarity 100.0%; Pred. No. 9,7e-65;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 AECPTLGEAVTDHPDRLNAMEKEFYVLDKQHAMLPITTEIKDRLQRLVLRREDVVLGRP 60
        |||
        2 AECPTLGEAVTDHPDRLNAMEKEFYVLDKQHAMLPITTEIKDRLQRLVLRREDVVLGRP 61
QY      61 MTPPTQIGSLLPIMMQLYPDGGRYSSDSSFWRVLVYHIKIDGVEDMLLELPDD 113
        |||
        62 MTPPTQIGSLLPIMMQLYPDGGRYSSDSSFWRVLVYHIKIDGVEDMLLELPDD 114
DB
```

RESULT 2

```
US-10-040-862-666
; Sequence 666, Application US/10040862
; Publication No. US20030078396A1
```

```
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
FILE REFERENCE: 014058-013520US
CURRENT FILING DATE: 2001-11-06
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-05-01
PRIOR FILING DATE: 2000-05-01
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-04
PRIOR FILING DATE: 2000-08-07
PRIOR FILING DATE: 2001-03-01
NUMBER OF SEQ ID NOS: 10467
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 666
LENGTH: 114
TYPE: PRT
ORGANISM: Homo sapiens
US-10-040-862-666
```

```
Query Match          100.0%; Score 612; DB 14; Length 114;
Best Local Similarity 100.0%; Pred. No. 9,7e-65;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 AECPTLGEAVTDHPDRLNAMEKEFYVLDKQHAMLPITTEIKDRLQRLVLRREDVVLGRP 60
        |||
        2 AECPTLGEAVTDHPDRLNAMEKEFYVLDKQHAMLPITTEIKDRLQRLVLRREDVVLGRP 61
QY      61 MTPPTQIGSLLPIMMQLYPDGGRYSSDSSFWRVLVYHIKIDGVEDMLLELPDD 113
        |||
        62 MTPPTQIGSLLPIMMQLYPDGGRYSSDSSFWRVLVYHIKIDGVEDMLLELPDD 114
DB
```

RESULT 3

```
US-10-057-475B-666
; Sequence 666, Application US/10057475B
; Publication No. US20040002068A1
```

```
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Clapper, Jonathan David
APPLICANT: Wang, Aijun
APPLICANT: Ordonez, Nadia
APPLICANT: Carter, Lauren
APPLICANT: McNeill, Patricia Dianne
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
FILE REFERENCE: 014058-014402US
CURRENT FILING DATE: 2002-01-22
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-05-01
PRIOR FILING DATE: 2000-05-01
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-22
PRIOR FILING DATE: 2000-05-22
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 10979
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 666
LENGTH: 114
TYPE: PRT
ORGANISM: Homo sapiens
US-10-057-475B-666
```

```
Query Match          100.0%; Score 612; DB 15; Length 114;
Best Local Similarity 100.0%; Pred. No. 9,7e-65;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 AECPTLGEAVTDHPDRLNAMEKEFYVLDKQHAMLPITTEIKDRLQRLVLRREDVVLGRP 60
        |||
        2 AECPTLGEAVTDHPDRLNAMEKEFYVLDKQHAMLPITTEIKDRLQRLVLRREDVVLGRP 61
QY      61 MTPPTQIGSLLPIMMQLYPDGGRYSSDSSFWRVLVYHIKIDGVEDMLLELPDD 113
        |||
        62 MTPPTQIGSLLPIMMQLYPDGGRYSSDSSFWRVLVYHIKIDGVEDMLLELPDD 114
DB
```

RESULT 4

```
US-10-154-884B-666
; Sequence 666, Application US/10154884B
```

```
Publication No. US20040005561A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc W.
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
FILE REFERENCE: 014058-013521US
CURRENT APPLICATION NUMBER: US/10/154,884B
CURRENT FILING DATE: 2002-05-23
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: US 60/218,950
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 60/222,903
PRIOR FILING DATE: 2000-08-03
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 11290
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 666
LENGTH: 114
TYPE: PRT
ORGANISM: Homo sapiens
US-10-154-884B-666

Query Match          100.0%; Score 612; DB 15; Length 114;
Best Local Similarity 100.0%; Pred. No. 9.7e-65;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AECPTLGAVTVDHPRLWAMEKFTVYLDEKQHAWLPITIEIKDRLOLRVLRREDVVLGRP 60
        |||||||
Db      2 AECPTLGAVTVDHPRLWAMEKFTVYLDEKQHAWLPITIEIKDRLOLRVLRREDVVLGRP 61
        |||||||

Qy      61 MTPQIGPSLLPIWMQLYPDGRYRSSDSSFWRVLYYHIKIDGVEDMLLELPDD 113
        |||||||
Db      62 MTPQIGPSLLPIWMQLYPDGRYRSSDSSFWRVLYYHIKIDGVEDMLLELPDD 114
        |||||||

RESULT 5
US-10-057-475B-10485
Sequence 10485, Application US/10057475B
Publication No. US20040002068A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Clapper, Jonathan David
APPLICANT: Wang, Aijun
APPLICANT: Ordenez, Nadia
APPLICANT: Carter, Lauren
APPLICANT: McNeill, Patricia Dianne
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
FILE REFERENCE: 014058-014402US
CURRENT APPLICATION NUMBER: US/10/057,475B
CURRENT FILING DATE: 2002-01-22
```

```
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: US 60/218,950
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 60/222,903
PRIOR FILING DATE: 2000-08-03
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 10979
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 10485
LENGTH: 121
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: His-TCL-1, TCL-1 with His tag
US-10-057-475B-10485

Query Match          100.0%; Score 612; DB 15; Length 121;
Best Local Similarity 100.0%; Pred. No. 1e-64;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AECPTLGAVTVDHPRLWAMEKFTVYLDEKQHAWLPITIEIKDRLOLRVLRREDVVLGRP 60
        |||||||
Db      9 AECPTLGAVTVDHPRLWAMEKFTVYLDEKQHAWLPITIEIKDRLOLRVLRREDVVLGRP 68
        |||||||

Qy      61 MTPQIGPSLLPIWMQLYPDGRYRSSDSSFWRVLYYHIKIDGVEDMLLELPDD 113
        |||||||
Db      69 MTPQIGPSLLPIWMQLYPDGRYRSSDSSFWRVLYYHIKIDGVEDMLLELPDD 121
        |||||||

RESULT 6
US-10-154-884B-10485
Sequence 10485, Application US/10154884B
Publication No. US20040005561A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc W.
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
FILE REFERENCE: 014058-013521US
CURRENT APPLICATION NUMBER: US/10/154,884B
CURRENT FILING DATE: 2002-05-23
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR FILING DATE: 2000-05-04
```

```

; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10485
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: His-TCL-1, TCL-1 with His tag
US-10-154-884B-10485

Query Match          100.0%; Score 612; DB 15; Length 121;
Best Local Similarity 100.0%; Pred. No. 1e-64;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 AECPTLGEAVTDHPDRLMAWEKFFVYLDEKQHAMLPITIEIKDRLQLRVLLRREDVYLGR 60
    |||
Db 9 AECPTLGEAVTDHPDRLMAWEKFFVYLDEKQHAMLPITIEIKDRLQLRVLLRREDVYLGR 68
    |||

Cy 61 MTPPIGSLPIMMQLYPDGRYSSDSSFWRLVYHIKIDGVEMLLELPDD 113
    |||
Db 69 MTPPIGSLPIMMQLYPDGRYSSDSSFWRLVYHIKIDGVEMLLELPDD 121
    |||

RESULT 7
US-09-796-692-1528
; Sequence 1528, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; FILE REFERENCE: 2077.001200
; CURRENT FILING DATE: US/09/796,692
; PRIOR APPLICATION NUMBER: 2001-03-01
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1528
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Homo sapiens
```

```

US-09-796-692-1528

Query Match          52.0%; Score 318; DB 9; Length 76;
Best Local Similarity 100.0%; Pred. No. 5.4e-30;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 AECPTLGEAVTDHPDRLMAWEKFFVYLDEKQHAMLPITIEIKDRLQLRVLLRREDVYLGR 59
    |||
Db 18 AECPTLGEAVTDHPDRLMAWEKFFVYLDEKQHAMLPITIEIKDRLQLRVLLRREDVYLGR 76
    |||

RESULT 8
US-10-040-862-1528
; Sequence 1528, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013520US
; CURRENT FILING DATE: US/10/040,862
; PRIOR APPLICATION NUMBER: 2001-11-06
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1528
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-040-862-1528

Query Match          52.0%; Score 318; DB 14; Length 76;
Best Local Similarity 100.0%; Pred. No. 5.4e-30;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 AECPTLGEAVTDHPDRLMAWEKFFVYLDEKQHAMLPITIEIKDRLQLRVLLRREDVYLGR 59
    |||
Db 18 AECPTLGEAVTDHPDRLMAWEKFFVYLDEKQHAMLPITIEIKDRLQLRVLLRREDVYLGR 76
    |||

RESULT 9
US-10-057-475B-1528
; Sequence 1528, Application US/10057475B
; Publication No. US20040002068A1
```

```

: GENERAL INFORMATION:
: APPLICANT: Gaiger, Alexander
: APPLICANT: Algate, Paul A.
: APPLICANT: Mannion, Jane
: APPLICANT: Clapper, Jonathan David
: APPLICANT: Wang, Aijun
: APPLICANT: Ordonez, Nadia
: APPLICANT: Carter, Lauren
: APPLICANT: McNeill, Patricia Dianne
: APPLICANT: Corixa Corporation
: TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
: TITLE OF INVENTION: Hematological Malignancies
: FILE REFERENCE: 014058-014402US
: CURRENT APPLICATION NUMBER: US/10/057,475B
: CURRENT FILING DATE: 2002-01-22
: PRIOR APPLICATION NUMBER: US 60/186,126
: PRIOR FILING DATE: 2000-03-01
: PRIOR APPLICATION NUMBER: US 60/190,479
: PRIOR FILING DATE: 2000-03-17
: PRIOR APPLICATION NUMBER: US 60/200,545
: PRIOR FILING DATE: 2000-04-27
: PRIOR APPLICATION NUMBER: US 60/200,303
: PRIOR FILING DATE: 2000-04-28
: PRIOR APPLICATION NUMBER: US 60/200,779
: PRIOR FILING DATE: 2000-04-28
: PRIOR APPLICATION NUMBER: US 60/200,999
: PRIOR FILING DATE: 2000-05-01
: PRIOR APPLICATION NUMBER: US 60/202,084
: PRIOR FILING DATE: 2000-05-04
: PRIOR APPLICATION NUMBER: US 60/206,201
: PRIOR FILING DATE: 2000-05-22
: PRIOR APPLICATION NUMBER: US 60/218,950
: PRIOR FILING DATE: 2000-07-14
: PRIOR APPLICATION NUMBER: US 60/222,903
: PRIOR FILING DATE: 2000-08-03
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 10979
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 1528
: LENGTH: 76
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-057-475B-1528

Query Match      52.0%; Score 318; DB 15; Length 76;
Beat Local Similarity 100.0%; Pred. No. 5,4e-30;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AECCTLGEAVTDHPDRRLWAMEKFFVYLDEKQHAMVPLTTEIQRILQRLVLRREDVIGR 59
DB      18 AECPTLGEAVTDHPDRRLWAMEKFFVYLDEKQHAMVPLTTEIQRILQRLVLRREDVIGR 76

RESULT 10
US-10-154-884B-1528
: Sequence 1528, Application US/10154884B
: Publication No. US20040005561A1
: GENERAL INFORMATION:
: APPLICANT: Gaiger, Alexander
: APPLICANT: Algate, Paul A.
: APPLICANT: Mannion, Jane
: APPLICANT: Retter, Marc W.
: APPLICANT: Corixa Corporation
: TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
: TITLE OF INVENTION: Hematological Malignancies
: FILE REFERENCE: 014058-013521US
: CURRENT APPLICATION NUMBER: US/10/154,884B
: CURRENT FILING DATE: 2002-05-23
: PRIOR APPLICATION NUMBER: US 60/186,126
: PRIOR FILING DATE: 2000-03-01
: PRIOR APPLICATION NUMBER: US 60/190,479
: PRIOR FILING DATE: 2000-03-17
: PRIOR APPLICATION NUMBER: US 60/200,545

```

```

P07689      1 PRIOR FILING DATE: 2000-04-27
P07689      2 PRIOR APPLICATION NUMBER: US 60/200,303
P07689      3 PRIOR FILING DATE: 2000-04-28
P07689      4 PRIOR APPLICATION NUMBER: US 60/200,779
P07689      5 PRIOR FILING DATE: 2000-04-28
P07689      6 PRIOR APPLICATION NUMBER: US 60/200,999
P07689      7 PRIOR FILING DATE: 2000-05-01
P07689      8 PRIOR APPLICATION NUMBER: US 60/202,084
P07689      9 PRIOR FILING DATE: 2000-05-04
P07689     10 PRIOR APPLICATION NUMBER: US 60/206,201
P07689     11 PRIOR FILING DATE: 2000-05-22
P07689     12 PRIOR APPLICATION NUMBER: US 60/218,950
P07689     13 PRIOR FILING DATE: 2000-07-14
P07689     14 PRIOR APPLICATION NUMBER: US 60/222,903
P07689     15 PRIOR FILING DATE: 2000-08-03
P07689     16 Remaining Prior Application data removed - See file wrapper or PALM.
P07689     17 NUMBER OF SEQ ID NOS: 11290
P07689     18 SOFTWARE: FastSeq for Windows Version 3.0
P07689     19 SEQ ID NO:1528
P07689     20 LENGTH: 76
P07689     21 TYPE: PRT
P07689     22 ORGANISM: Homo sapiens
P07689     23 US-10-154-884B-1528

Query Match          52.0%; Score 318; DB 15; Length 76;
Best Local Similarity 100.0%; Pident. No. 5,4e-30;
Matches    59; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

Cy       1 AECPTLGEAATVDDHDPRLAMWKKFYVLDEKQAMLTPLTEIKDRIQLTVLARREPVYIGR 59
Db       18 AECPTLGSAVTVDHPDRLMWEKFYVLDEKQHAWLPLETEIKDRIQLTVLARLRREDVILGR 76

RESULT 11
US-10-282-122A-56015
Sequence 56015, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zykkind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITTA 03AA
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: US/10/282,122A
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308

```

```

? PRIOR FILING DATE: 2001-02-16
? Remaining Prior Application data removed - see File Wrapper or PALM.
? NUMBER OF SEQ ID NOS: 78614
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO: 56015
?
? LENGTH: 621
?
? TYPE: PRAT
? ORGANISM: Enterobacter cloacae
?
? US-10-282-122A-56015

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Query Match 15.0%; Score 92; DB 12; Length 621;  
 Best Local Similarity 33.3%; Pred. No. 0.057;  
 Matches 25; Conservative 16; Mismatches 26; Indels 8; Gaps 3;

[illegible]

## RESULT 12

US-10-282-122A-68466  
Seminence 68466 Application IRS/10282122A

Publication No. US20040029129A1

Query Match	15.0%;	Score 91.5;	DB 12;	Length 625;
Best Local Similarity	33.3%;	Pred. No. 0.066;		
Matches 26;	Conservative 13;	Mismatches 24;	Indels 15;	Gaps 4;

```

0y      16 RNAMEKPYVLD-----KOHAMLEPLTI-----EIKDRLOQLRVLLREDVDVLCGRMPTQ 65
      : ||| | | | : : : | | | | | |
Db      441 KTNAMW--TALDQLRSEESQSLIRIRIGDPAGVR--LVVDVLRREITVFEPLMTLIP 499

```

```
QY      66  IGPSLLPIMWQLYPDGRY  83
          ::|||:||||:|
Db      496 SNKALPLIMQLFPDNPY  513
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RESULT 13  
US-10-282

Sequence 75406, Application US/10282122A  
Publication No. US20040039139A1

; GENERAL INFORMATION:

ORGANISM: *Salmonella typhi*  
US-10-282-122A-75406

Query Match	14.1%	Score 86;	DB 12;	Length 618;
Best Local Similarity	29.7%;	Pred. No. 0.29;		
Matches	22;	Conservative	20;	Mismatches 26;
				Indels 6;
				Gaps 3
16 RUMAM-----EKEFYVLDEKQHAMLP-L-TIEIKDRLQLRVLRREDVVLGRPW-TTPQIGPS	69			

QY 70 L L P I M W Q L Y P D G R Y 83  
: | | : | | : | |



[illegible]

```

: Publication No. US20040029129A1
: GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zykkind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
: TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
: FILE REFERENCE: ELITRA.034A
: CURRENT FILING DATE: 2003-02-20
: PRIOR APPLICATION NUMBER: 60/1191,078
: PRIOR FILING DATE: 2000-03-21
: PRIOR APPLICATION NUMBER: 60/206,848
: PRIOR FILING DATE: 2000-05-23
: PRIOR APPLICATION NUMBER: 60/207,727
: PRIOR FILING DATE: 2000-05-26
: PRIOR APPLICATION NUMBER: 60/230,335
: PRIOR FILING DATE: 2000-09-06
: PRIOR APPLICATION NUMBER: 60/230,347
: PRIOR FILING DATE: 2000-09-09
: PRIOR APPLICATION NUMBER: 60/242,578
: PRIOR FILING DATE: 2000-10-23
: PRIOR APPLICATION NUMBER: 60/253,625
: PRIOR FILING DATE: 2000-11-27
: PRIOR APPLICATION NUMBER: 60/257,931
: PRIOR FILING DATE: 2000-12-22
: PRIOR APPLICATION NUMBER: 60/267,636
: PRIOR FILING DATE: 2001-02-09
: PRIOR APPLICATION NUMBER: 60/269,308
: PRIOR FILING DATE: 2001-02-16
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 78614
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 43135
: LENGTH: 619
: TYPE: PRT
: ORGANISM: Escherichia coli
US-10-282-122A-43135

Query Match      13.6%; Score 83; DB 12; Length 619;
Best Local Similarity 28.4%; Pred. No. 0.67;
Matches 21; Conservative 21; Mismatches 26; Indels 6; Gaps 3

QY 16 RLMWME---KFLVYDEKONHMLPL-TLEIKRRLQLRLRREDVVLGRPM-TPTQIGPS 69
      : ||||| : : : : : : : : : : : : : : : : : : : : : : : : :
Db 440 KTWAMEAFAPQDIRVSDRFAVAVIRKIGHPONEVRLIDVLRLPEVLYEPRMLTVIPGSKA 499
      : ||||| : : : : : : : : : : : : : : : : : : : : : : : : :
QY 70 LRLPMQQLYDPGRY 83
      : ||||| : : : : : : : : : : : : : : : : : : : : : : : : :
Db 500 ILPLIMSLFPHNRY 513

Search completed: June 17, 2004, 14:37:31
Job time : 503 secs

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*This Page Blank (uspto)*

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 17, 2004, 14:25:11 ; Search time 22 Seconds  
(without alignments)  
265.170 Million cell updates/sec

Title: US-09-441-242a-2

Perfect score: 612

Sequence: 1 AECPTLGEAVTDHPDRLMAW.....VYHKKIDGVEDMLLELPDD 113

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	612	100.0	113	2	US-08-330-272-2
2	612	100.0	113	5	PCT-US95-13663-2
3	221	36.1	108	2	US-08-330-272-4
4	221	36.1	108	5	PCT-US95-13663-4
5	91.5	15.0	639	4	US-09-543-681A-6148
6	83	13.6	621	4	US-09-489-039A-9256
7	74	12.1	363	4	US-09-549-848B-39
8	67	10.9	206	2	US-08-438-439C-19
9	66	10.8	256	3	US-08-484-905-113
10	66	10.8	256	3	US-08-481-985B-113
11	66	10.8	256	3	US-08-376-476-113
12	66	10.8	500	3	US-08-960-190A-25
13	65	10.6	712	4	US-09-489-039A-10736
14	64	10.5	194	4	US-09-107-532A-6568
15	64	10.5	344	4	US-09-198-452A-880
16	63.5	10.4	489	4	US-09-310-463-14
17	63.5	10.4	489	4	US-08-842-248A-14
18	63.5	10.4	906	1	US-08-220-151-9
19	63.5	10.4	906	1	US-08-413-118-9
20	63.5	10.4	906	3	US-08-473-446-9
21	63.5	10.4	1019	1	US-08-296-014A-4
22	63.5	10.4	1019	2	US-08-596-405-4
23	63.5	10.4	1019	2	US-08-877-620-4
24	63.5	10.4	1019	4	US-09-287-368-4
25	63.5	10.4	1083	1	US-08-296-014A-2
26	63.5	10.4	1083	2	US-08-596-405-2
27	63.5	10.4	1083	2	US-08-877-620-2

28	63.5	10.4	1083	4	US-09-287-368-2	Sequence 2, Appli
29	62.5	10.2	382	4	US-09-489-039A-8323	Sequence 8323, Ap
30	62	10.1	509	3	US-08-890-980-2	Sequence 2, Appli
31	62	10.1	509	3	US-08-890-979-2	Sequence 2, Appli
32	62	10.1	509	3	US-09-032-894-2	Sequence 2, Appli
33	62	10.1	509	3	US-09-031-626-2	Sequence 23905, A
34	62	10.1	703	4	US-09-252-991A-23905	Sequence 6, Appli
35	61.5	10.0	713	1	US-08-453-472-6	Sequence 7, Appli
36	61.5	10.0	713	1	US-08-038-948-7	Sequence 8, Appli
37	61.5	10.0	713	1	US-08-038-948-8	Sequence 10, Appli
38	61.5	10.0	713	1	US-08-038-948-10	Sequence 6, Appli
39	61.5	10.0	713	2	US-08-453-952-6	Sequence 6, Appli
40	61.5	10.0	713	2	US-08-862-903-6	Sequence 22189, A
41	61	10.0	222	4	US-09-252-991A-22189	Sequence 27705, A
42	61	10.0	546	4	US-09-252-991A-27705	Sequence 2, Appli
43	61	10.0	785	3	US-09-265-108-2	Sequence 2, Appli
44	61	10.0	785	3	US-09-479-264-2	Sequence 13602, A
45	61	10.0	1279	4	US-09-489-039A-13602	

ALIGNMENTS

RESULT 1  
US-08-330-272-2  
; Sequence 2, Application US/08330272  
; Patent No. 5985598  
; GENERAL INFORMATION:  
; APPLICANT: Russco et al  
; TITLE OF INVENTION: TCL-1 Gene and Protein and Related  
; TITLE OF INVENTION: Methods and Compositions  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edwards  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/330.272  
; FILING DATE:  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Miarock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 6754-027  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 790-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 113 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-330-272-2  
Query Match 100.0%; Score 612; DB 2; length 113;  
Best Local Similarity 100.0%; Pred. No. 8.1e-71;  
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Cy 1 AECPTLGEAVTDHPDRLMAWEKFFYLDEKQAAVPLTIEIKDRLOQLVLRREDVYVGRP 60  
Db 1 AECPTLGEAVTDHPDRLMAWEKFFYLDEKQAAVPLTIEIKDRLOQLVLRREDVYVGRP 60  
Cy 61 MTPQIGPSLLPIWMOQLYPDGRYRSDSSFFRLVYVHKIDGVEDMLLELPDD 113

Db 61 MPTQIGPSLPIIMQLYPDGRYSSDSFMRVYHIKIDGVEDMLLELPDD 113

RESULT 2  
PCT-US95-13663-2  
Sequence 2, Application PC/TUS9513663  
GENERAL INFORMATION:  
APPLICANT: Russo et al  
TITLE OF INVENTION: TCL-1 Gene and Protein and Related  
TITLE OF INVENTION: Methods and Compositions  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/13663  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 6754-027  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 790-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 113 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US95-13663-2

Query Match 100.0%; Score 612; DB 5; Length 113;  
Best Local Similarity 100.0%; Pred. No. 8,1e-71;  
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 AECPTLGBAVTDHPDRLIMAEKFVYLDEKOHAMLPITIEIKDRLQLRVLRRREDVVLGRP 60  
1 AECPTLGBAVTDHPDRLIMAEKFVYLDEKOHAMLPITIEIKDRLQLRVLRRREDVVLGRP 60

Db 61 MPTQIGPSLPIIMQLYPDGRYSSDSFMRVYHIKIDGVEDMLLELPDD 113  
61 MPTQIGPSLPIIMQLYPDGRYSSDSFMRVYHIKIDGVEDMLLELPDD 113

RESULT 3  
US-08-330-272-4  
Sequence 4, Application US/08330272  
Patent No. 5985598  
GENERAL INFORMATION:  
APPLICANT: Russo et al  
TITLE OF INVENTION: TCL-1 Gene and Protein and Related  
TITLE OF INVENTION: Methods and Compositions  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/330,272  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 6754-027  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 790-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 108 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-330-272-4

Query Match 36.1%; Score 221; DB 2; Length 108;  
Best Local Similarity 40.2%; Pred. No. 1,1e-20;  
Matches 43; Conservative 23; Mismatches 39; Indels 2; Gaps 1;

Db 7 GEAVTDHPDRLIMAEKFVYLDEKOHAMLPITIEIKDRLQLRVLRRREDVVLGRPMPPTOI 66  
3 GEVGAHPDRLIMQYBERYMDNNSRLMQIHHLMVGVQELLKLPLPD 60

Db 67 GPSLPIIMQLYPDGRYSSDSFMRVYHIKIDGVEDMLLELPDD 113  
61 LTSQLPIIMQLYBERYMDNNSRLMQIHHLMVGVQELLKLPLPD 107

RESULT 4  
PCT-US95-13663-4  
Sequence 4, Application PC/TUS9513663  
GENERAL INFORMATION:  
APPLICANT: Russo et al  
TITLE OF INVENTION: TCL-1 Gene and Protein and Related  
TITLE OF INVENTION: Methods and Compositions  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/13663  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 6754-027  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 790-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:

ORGANISM: *Klebsiella pneumoniae*  
US-09-489-039A-9256

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;
;      200;
;      COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/438,439C  
FILING DATE: May 12, 1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Haile, Lisa A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 07265/046001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619/678-5070  
TELEFAX: 619/678-5099  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 206 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-438-439C-19

Query Match 10.9%; Score 67; DB 2; Length 206;  
Best Local Similarity 24.1%; Pred. No. 1.5;  
Matches 26; Conservative 6; Mismatches 30; Indels 46; Gaps 4;

QY 18 WAWKEPYLDEKQAMPLTEIKDRQLRLREDDVVGKPMTPQIGSLPIMW-- 75  
DB 45 WWMESLVAL---SLAMLPVAAQPKR-----AAVQAGAGYLLGIRKLMW 84

QY 76 -----QLYPDGRYRSSDSPFRVLVYHIKIDGVEDMLLELP 111  
DB 85 WLYCNVIGIHFHQLPDMGICGALADTW-----DSLLELSP 120

RESULT 9  
US-08-484-905-113  
Sequence 113, Application US/08484905  
Patent No. 5976551  
GENERAL INFORMATION:  
APPLICANT: Mottez, Estelle  
APPLICANT: Abastado, Jean-Pierre  
APPLICANT: Kourileky, Philippe  
TITLE OF INVENTION: An Altered Major Histocompatibility  
TITLE OF INVENTION: Complex (MHC) Determinant and Methods for Using the  
NUMBER OF INVENTION: Determinant  
NUMBER OF SEQUENCES: 127  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESS: Dunner  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington  
STATE: D.C.  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy Disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,905  
FILING DATE: 07-JUNE-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/801,818  
FILING DATE: 05-DEC-1991  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/792,473  
FILING DATE: 15-NOV-1991  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Potter, Jane E. R.

REGISTRATION NUMBER: 33,332  
REFERENCE/DOCKET NUMBER: 03495.0106-03000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 113:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 256 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-484-905-113

Query Match 10.8%; Score 66; DB 2; Length 256;  
Best Local Similarity 22.2%; Pred. No. 2.8;  
Matches 32; Conservative 24; Mismatches 30; Indels 58; Gaps 8;

QY 23 FYVDEKQAM-LPLTEIK-----DRLQLRLRED----- 54  
DB 60 YVDLKKETVWMLPEFAQLRRFPQGLQNIATGKHLBITLRKSNSTPATNEAPQATVF 119

QY 55 -----VILGRPMT-----PTQIGPSLLPIMW-----QLYPDGRYRS-----DSFWRU----- 93  
DB 120 PKSPVLLGQENTLICEFDNIFPPVINITWLRNSKSVTDGVYETSFVYNRDYSFKLSYLT 179

QY 94 -----VYHIKID--GVEDMLLE 108  
DB 180 FIPSDDIYDCKVEHMGLEBPVLK 203

RESULT 10  
US-08-481-985B-113  
Sequence 113, Application US/08481985B  
Patent No. 601146  
GENERAL INFORMATION:  
APPLICANT: Mottez, Estelle  
APPLICANT: Abastado, Jean-Pierre  
APPLICANT: Kourileky, Philippe  
TITLE OF INVENTION: Altered Major Histocompatibility Complex  
TITLE OF INVENTION: Determinant  
NUMBER OF SEQUENCES: 148  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESS: Dunner  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington  
STATE: D.C.  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/481,985B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/801,818  
FILING DATE: 05-DEC-1991  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/792,473  
FILING DATE: 15-NOV-1991  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 03495.0106-04000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 113:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 256 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-481-985B-113

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Query Match	10.8%	Score 66	DB 3	Length 256
Best Local Similarity	22.2%	Pred. No. 2.8		
Matches 32; Conservative	24	Mismatches 30	Indels 58	Gaps 8

```

QY      23 FVYLDEKQAM-LELTETK-----DELQRYLLRED-----54
      60 YVDLDEKETVMLEPAQLRRPEPGGLGNIATGHNLEILTKSNSTPATNEAPQATVP 119
Db      55 ----VVLGRPMT-----PTQIGPSLLPIWM----QLYDGRYSS----DSSFARL-----93
      120 KPSVLLGQPNITICFVDNIFFPVNIITWLNRKNSVTDGVETETSFVNRDYSFHKLSYLT 179
Db      94 -----VYHKID--GVEDMLE 108
      180 FIPSDDIYDCKVEHNGLEEPVLK 203

```

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1 RESULT 11
2 US-08-370-476-113
3 Sequence 113 Application US/08370476
4 Patent No. 6153408
5 GENERAL INFORMATION:
6 APPLICANT: Mottez, Estelle
7 APPLICANT: Abastado, Jean-Pierre
8 APPLICANT: Kouzileky, Philippe
9 APPLICANT: Lone, Yu-Chun
10 APPLICANT: Ocius, David
11 APPLICANT: Carrouge, Armand
12 TITLE OF INVENTION: Altered Major Histocompatibility Complex
13 TITLE OF INVENTION:
14 NUMBER OF SEQUENCES: 127
15 CORRESPONDENCE ADDRESS:
16 ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
17 ADDRESSEE: Dunner
18 STREET: 1300 I Street, N.W., Suite 700
19 CITY: Washington
20 STATE: D.C.
21 ZIP: 20005-3315
22 COMPUTER READABLE FORM:
23 MEDIUM TYPE: IBM PC compatible
24 COMPUTER: IBM PC compatible
25 OPERATING SYSTEM: PC-DOS/MS-DOS
26 SOFTWARE: PatentIn Release #1.0, Version #1.25
27 CURRENT APPLICATION DATA:
28 APPLICATION NUMBER: US/08/370,476
29 FILING DATE:
30 CLASSIFICATION: 435
31 PRIOR APPLICATION DATA:
32 APPLICATION NUMBER: US 08/117,575
33 FILING DATE: 07-SEP-1993
34 APPLICATION NUMBER: US 08/072,767
35 FILING DATE: 06-JUN-1993
36 PRIOR APPLICATION DATA:
37 APPLICATION NUMBER: US 07/801,818
38 FILING DATE: 05-DEC-1991
39 PRIOR APPLICATION DATA:
40 APPLICATION NUMBER: US 07/792,473
41 FILING DATE: 15-NOV-1991
42 ATTORNEY/AGENT INFORMATION:
43 NAME: Meyers, Kenneth J.
44 REGISTRATION NUMBER: 25,146
45 REFERENCE/DOCKET NUMBER: 05243.0001-01000
46 TELECOMMUNICATION INFORMATION:
47 TELEPHONE: 202-408-4000
48 TELEFAX: 202-408-4400
49 INFORMATION FOR SEQ ID NO: 113:

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; SEQUENCE CHARACTERISTICS:
;     LENGTH: 256 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;     MOLECULE TYPE: peptide
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US-08-370-476-113

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Query Match	10.8%;	Score 66;	DB 3;	Length 256;
Best Local Similarity	22.2%;	Pred. NO. 2.8;		
Matches	32;	Conservative	24;	Mismatches 30;
				Indels 58;
				Gaps 8;

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QY      23 FVYLDEKQHAW-LPTLTIEK-----DRIGLRVLRRRD-----54  
       :|::||:::||:  
Db     60 YVDLDDKEETVMMLPEFAQLRREPEROGGLONATGSHNLEITTKSNSTPATNEAPQAIVF   119  
  
QY      55 ----VVIAGRPMT----PFIGPSLLPIWM---OLYPDGRYSRS--DSFPRL- ---93  
       |||||::|::||  
Db    120 PKSFVLLGGPNTLICFDVNIPPPVINIWTLMNSKSVTDGVEITSFFVRNDISPFKLSYLT   179  
  
QY      94 -----VVHIKID--GVEDMMLE 108  
       ::||::|::||:  
Db    180 FIIPSDDDIYDCCKEHHMGLEEPAVLK 203
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RESULT 12
US-08-960-190A-25
Sequence 25, Application US/08960190A
Patent No. 6232445
GENERAL INFORMATION:
APPLICANT: Rhode, Peter R.
APPLICANT: Acevedo, Jorge
APPLICANT: Burkhart, Martin
APPLICANT: Jiao, Jin-an
APPLICANT: Wong, Hing C.
TITLE OF INVENTION: SOLUBLE MHC COMPLEXES AND
TITLE OF INVENTION: METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESSES:
ADDRESSES: Dike, Bronstein, Roberts & Cushman, LLP
STREET: 130 Water Street
City: Boston
STATE: MA
COUNTRY: usa
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PACESEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/960,190A
FILING DATE: 29-OCT-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Corleas, Peter F
REGISTRATION NUMBER: 33,860
REFERENCE/DOCKET NUMBER: 448002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX:
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 500 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-960-190A-25

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; APPLICATION NUMBER: US/09/107,5532A
; FILING DATE:30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneké
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6568:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 194 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (8) LOCATION 1..194
; SEQUENCE DESCRIPTION: SEQ ID NO: 6568:
US-09-107-5532A-6568

Query Match 10.5%; Score 64; DB 4; Length 194;
Best Local Similarity 26.8%; Pred. No. 3.4;
Matches 30; Conservative 14; Mismatches 34; Indels 34; Gaps 9;

Y 7 GEAVTDHPRLWMEKFVYLD-EKOHAWLPLTIEIKRLQLRVLLRREDVVLGRPTPTQ 65
D 59 GATTAADHP---LIEPTYIEVDLENQHMWY-----YKDG---KVAL-ETDIVSGKPTTPT- 105
Y 66 IGPSLDPLTMQ-----LYPDGRYRSSDSFRLVNHKID---GYED 104
D 106 --PAGVFVWNKEEDATLKGINDGTPYSPVNVW-----MPLDWTGVGIHD 150

RESULT 15
US-09-198-452A-880
; Sequence 880, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 880
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-880

Query Match 10.5%; Score 64; DB 4; Length 344;
Best Local Similarity 31.4%; Pred. No. 7.4;
Matches 27; Conservative 11; Mismatches 24; Indels 24; Gaps 5;

Y 4 PTLGAAVVDHP-----RLWME-----KRVYIDKQOHAWLPL-----TIEIKDR 43
D 233 PLLLEAVLDHPAYRETSLLRDGIWEAVKRQEHAIQEHGQAAALELFTKRTDFRLRLDK 292
Y 44 LQLRVLLRREDV--VLGRPTPTQIG 67
D 293 MOL--LISRYDLLPLINKKMPDYTLG 316

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Search completed: June 17, 2004, 14:29:00  
Job time : 23 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 17, 2004, 11:25:55 ; Search time 3768 Seconds  
(without alignments)  
10492.974 Million cell updates/sec

Title: US-09-441-242a-1  
Perfect score: 1324  
Sequence: 1 ctgagagagcctgctctt.....catggaataaaaaaa 1324

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues  
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: em\_earth: \*  
2: em\_earth: \*  
3: em\_earth: \*  
4: em\_earth: \*  
5: em\_earth: \*  
6: em\_earth: \*  
7: em\_earth: \*  
8: em\_earth: \*  
9: gb\_earth: \*  
10: gb\_earth: \*  
11: gb\_earth: \*  
12: gb\_earth: \*  
13: gb\_earth: \*  
14: gb\_earth: \*  
15: em\_earth: \*  
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20: em\_earth: \*  
21: em\_earth: \*  
22: em\_earth: \*  
23: em\_earth: \*  
24: em\_earth: \*  
25: em\_earth: \*  
26: em\_earth: \*  
27: em\_earth: \*  
28: gb\_earth: \*  
29: gb\_earth: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result	No.	Score	Query	Match	Length	ID	Description
1	962	72.7	1029	9	AL560721	AL560721	AL560721
2	952	71.9	1023	9	AL560722	AL560722	AL560722
3	941.4	71.1	1201	13	BX421512	BX421512	BX421512
4	921	69.6	1043	12	BM927381	BM927381	BM927381

5	905.4	68.4	1031	13	B061021	B061021	AGENCOURT
6	903	68.2	985	13 <th>B062796</th> <th>B062796</th> <th>AGENCOURT</th>	B062796	B062796	AGENCOURT
7	889.8	67.2	986	13 <th>B065603</th> <th>B065603</th> <th>AGENCOURT</th>	B065603	B065603	AGENCOURT
8	886.6	67.0	1029	13 <th>B061232</th> <th>B061232</th> <th>AGENCOURT</th>	B061232	B061232	AGENCOURT
9	881.4	66.6	982	13 <th>B056675</th> <th>B056675</th> <th>AGENCOURT</th>	B056675	B056675	AGENCOURT
10	877.8	66.3	964	12 <th>B0754764</th> <th>B0754764</th> <th>AGENCOURT</th>	B0754764	B0754764	AGENCOURT
11	875	66.1	1056	13 <th>BM927621</th> <th>BM927621</th> <th>AGENCOURT</th>	BM927621	BM927621	AGENCOURT
12	870.4	65.7	988	13 <th>B0064806</th> <th>B0064806</th> <th>AGENCOURT</th>	B0064806	B0064806	AGENCOURT
13	858.2	64.8	990	13 <th>B0059785</th> <th>B0059785</th> <th>AGENCOURT</th>	B0059785	B0059785	AGENCOURT
14	858.2	64.8	1024	12 <th>BM927418</th> <th>BM927418</th> <th>AGENCOURT</th>	BM927418	BM927418	AGENCOURT
15	856.6	64.7	1038	12 <th>BM927384</th> <th>BM927384</th> <th>AGENCOURT</th>	BM927384	BM927384	AGENCOURT
16	849.2	64.1	1004	13 <th>BX407882</th> <th>BX407882</th> <th>AGENCOURT</th>	BX407882	BX407882	AGENCOURT
17	847.8	64.0	1003	13 <th>B0061891</th> <th>B0061891</th> <th>AGENCOURT</th>	B0061891	B0061891	AGENCOURT
18	845	63.8	990	13 <th>B0058531</th> <th>B0058531</th> <th>AGENCOURT</th>	B0058531	B0058531	AGENCOURT
19	834	63.0	1037	13 <th>B0055518</th> <th>B0055518</th> <th>AGENCOURT</th>	B0055518	B0055518	AGENCOURT
20	833.2	62.9	1026	13 <th>B0061686</th> <th>B0061686</th> <th>AGENCOURT</th>	B0061686	B0061686	AGENCOURT
21	832.4	62.9	905	13 <th>BQ882730</th> <th>BQ882730</th> <th>AGENCOURT</th>	BQ882730	BQ882730	AGENCOURT
22	829.2	62.6	963	13 <th>B0063405</th> <th>B0063405</th> <th>AGENCOURT</th>	B0063405	B0063405	AGENCOURT
23	826.6	62.4	982	13 <th>B0057145</th> <th>B0057145</th> <th>AGENCOURT</th>	B0057145	B0057145	AGENCOURT
24	826.4	62.4	894	12 <th>BG758818</th> <th>BG758818</th> <th>AGENCOURT</th>	BG758818	BG758818	AGENCOURT
25	826.2	62.4	1073	13 <th>B0065790</th> <th>B0065790</th> <th>AGENCOURT</th>	B0065790	B0065790	AGENCOURT
26	825.8	62.4	1030	13 <th>B0061108</th> <th>B0061108</th> <th>AGENCOURT</th>	B0061108	B0061108	AGENCOURT
27	823.8	62.2	988	13 <th>BQ060743</th> <th>BQ060743</th> <th>AGENCOURT</th>	BQ060743	BQ060743	AGENCOURT
28	823	62.2	1002	13 <th>BX407883</th> <th>BX407883</th> <th>AGENCOURT</th>	BX407883	BX407883	AGENCOURT
29	822.8	62.1	1030	13 <th>B0066787</th> <th>B0066787</th> <th>AGENCOURT</th>	B0066787	B0066787	AGENCOURT
30	819.8	61.9	1001	13 <th>B0060857</th> <th>B0060857</th> <th>AGENCOURT</th>	B0060857	B0060857	AGENCOURT
31	818.2	61.8	952	13 <th>B0064150</th> <th>B0064150</th> <th>AGENCOURT</th>	B0064150	B0064150	AGENCOURT
32	815.8	61.6	876	13 <th>BX435946</th> <th>BX435946</th> <th>AGENCOURT</th>	BX435946	BX435946	AGENCOURT
33	813.8	61.5	975	12 <th>BG759376</th> <th>BG759376</th> <th>AGENCOURT</th>	BG759376	BG759376	AGENCOURT
34	813.6	61.5	982	13 <th>B0061994</th> <th>B0061994</th> <th>AGENCOURT</th>	B0061994	B0061994	AGENCOURT
35	811.2	61.3	916	12 <th>BG757301</th> <th>BG757301</th> <th>AGENCOURT</th>	BG757301	BG757301	AGENCOURT
36	807.8	61.0	1040	13 <th>B0056512</th> <th>B0056512</th> <th>AGENCOURT</th>	B0056512	B0056512	AGENCOURT
37	804.8	60.8	963	13 <th>B0063369</th> <th>B0063369</th> <th>AGENCOURT</th>	B0063369	B0063369	AGENCOURT
38	802.8	60.6	1004	13 <th>BQ064800</th> <th>BQ064800</th> <th>AGENCOURT</th>	BQ064800	BQ064800	AGENCOURT
39	796	60.4 <td>883</td> <td>13<th>BX443335</th><th>BX443335</th><th>AGENCOURT</th></td>	883	13 <th>BX443335</th> <th>BX443335</th> <th>AGENCOURT</th>	BX443335	BX443335	AGENCOURT
40	795	60.0 <td>863</td> <td>12<th>BM051836</th><th>BM051836</th><th>AGENCOURT</th></td>	863	12 <th>BM051836</th> <th>BM051836</th> <th>AGENCOURT</th>	BM051836	BM051836	AGENCOURT
41	794	60.0 <td>1018</td> <td>13<th>BQ063070</th><th>BQ063070</th><th>AGENCOURT</th></td>	1018	13 <th>BQ063070</th> <th>BQ063070</th> <th>AGENCOURT</th>	BQ063070	BQ063070	AGENCOURT
42	793.8	60.0 <td>927</td> <td>13<th>BQ643245</th><th>BQ643245</th><th>AGENCOURT</th></td>	927	13 <th>BQ643245</th> <th>BQ643245</th> <th>AGENCOURT</th>	BQ643245	BQ643245	AGENCOURT
43	793.6	59.9	1022	12 <th>B0054660</th> <th>B0054660</th> <th>AGENCOURT</th>	B0054660	B0054660	AGENCOURT
44	793	59.9	978	13 <th>BQ057729</th> <th>BQ057729</th> <th>AGENCOURT</th>	BQ057729	BQ057729	AGENCOURT
45	790.8	59.7	795	12 <th>B1226543</th> <th>B1226543</th> <th>AGENCOURT</th>	B1226543	B1226543	AGENCOURT

## ALIGNMENTS

RESULT 1  
AL560721/c  
LOCUS  
DEFINITION AL560721 Homo sapiens B CELLS (BAMOS CELL LINE) COT 25-NORMALIZED  
ACCESSION Homo sapiens CDNA clone CSODL0041M02 3-PRIME, mRNA sequence.  
VERSION AL560721  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 7222.r for  
more information about this cluster, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CSODL0041M02INP1cluster=7222.r. Contact :  
Feng Liang Email: fliang@lifetech.com URL :  
On Feb 15, 2001 this sequence version replaced gi:12907452.

http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Faraday Avenue Genoscope sequence ID : CS0DL004BG01NP1.

ORIGIN

Query Match	72.7%;	Score 962;	DB 9;	Length 1029;
Best Local Similarity	97.8%;	Pred. No. 1.6e-189;		
Matches 1009; Conservative	8;	Mismatches 10;	Indels 5;	Gaps 4

Qy	155	TAACATCAAGATTAAGATAGATTACGTTACGGGTCCTTGGTCGGGAAGAAGCTCG	214
Db	1029	TAACATCAAGATTAAGATAGATTACGTTACGGGTCCTTGGTCGGGAAGAAGCTCG	970
Qy	215	TCCTGGGAGGCGCTATGACCCCGACCGATAGGCCCAAGCGCTGCTCATCATGTGGC	274
Db	969	TCCTGGGAGGCGCTATGACCCCGACCGATAG--CCCAAGCTGCTCATCATGTGGC	912
Qy	275	AGCTCAACCTGATGAGCATACCGATCTCGAGCTCCAGTTTCTGGCGCTTAGTGTACC	334
Db	911	AGCTCAACCTGATGAGCATACCGATCTCGAGCTCCAGTBTGCGCTTTATGTACC	852
Qy	335	ACATCAAGATTAGCGCGGTGAGAGCATGTTCTCGAGCTGCTGCCAGATGACGATGTGA	394
Db	851	ACATCAAGATTAGCGCGGTGAGAGCATGTTCTCGAGCTGCTGCCAGATGACGATGTGA	792
Qy	395	TGGTCTTGGCAGACCTGTCTCTCTTCA-CCCAAGGCGTGAAGCTGCGCAGCTCAAT	453
Db	791	TGGTCTTGGCAGACCTGTCTCTCTTCA-CCCAAGGCGTGAAGCTGCGCAGCTCAAT	732
Qy	454	GGGAGATGTGTGTCTGTTCACCTTGTTACCTGCTGTGTCTTCTCCACCAAGCTG	513
Db	731	GGGAGATGTGTGTCTGTTCACCTTGTTACCTGCTGTGTCTTCTCCACCAAGCTG	672
Qy	514	GGGCTGGGAGGAATGAGCAGACAGAGATAGGCTTACCCAGGCGCTGAGAGACTGGC	573
Db	671	GGGCTGGGAGGAATGAGCAGACAGAGATAGGCTTACCCAGGCGCTGAGAGACTGGC	612
Qy	574	TGTAGCCCACTGTGCTGCGCTTAGACATACCACTCTGCCAAGAGGATTCACATTGGGA	633
Db	611	TGTAGCCCACTGTGCTGCGCTTAGACATACCACTCTGCCAAGAGGATTCACATTGGGA	552
Qy	634	GAGCTTCTTCCAGGTGCGCAGATATCCTGTGCTCGACTTTTCTCAGCTGATGTGT	693
Db	551	GAGCTTCTTCCAGGTGCGCAGATATCCTGTGCTCGACTTTTCTCAGCTGATGTGT	492
Qy	694	CTTGAAGCCCTTTCGTGCCCTTCTGTGCCCTCAGACGATAGTATTTCACTGTGCAACCC	753
Db	491	CTTGAAGCCCTTTCGTGCCCTTCTGTGCCCTCAGACGATAGTATTTCACTGTGCAACCC	432
Qy	754	ACTCAGCTCCGTGAACCTGTGAGAAACAGCGCATTAACCTGAGCAGAGACCTGTGAACC	813
Db	431	ACTCAGCTCCGTGAACCTGTGAGAAACAGCGCATTAACCTGTGAGCAGAGACCTGTGAACC	372
Qy	814	CTGAGCAAGTGTCTCACATGTGTCTACGCTGTGATGTAAACAAGCTGTCAACGCTGCG	873
Db	371	CTGAGCAAGTGTGTCTCACATGTGT-STRAGCTGTGATGTAAACAAGCTGTCAACGCTGCG	313
Qy	874	TGCCGCTAAACAAGCTGTGCAAAAGCTGTGCGCTGCCCTGTAAACAAGCTGTGAACGCTGCTG	933
Db	312	TGCCGCTAAACAAGCTGTGCAAAAGCTGTGCGCTGCCCTGTAAACAAGCTGTGAACGCTGCTG	253

QY	934	CCCAACACAGGTTCAACGTACAGTCAAGAAAGCCCTGAAGAAGCCCTTATCTGTGCTCA	993
Db	252	CCCAACACAGTTCACTGACAGTCAAGAAAGCCCTGAAGAGCCCTTATCTGTGCTCA	193
QY	994	GGACTCAGAAAGCCTCTGGGTCAGTGTCACATCCGGAGCAGCAGAGAGCCAGGCGG	1053
Db	192	GGACTCAGAAAGCCTCTGGGTCAGTGTCACATCCGGAGCAGCAGAGAGCCAGGCGG	133
QY	1054	GCGAGCCCTGTGAGATGAGCCCTCAGAACCCCTTGGCTTGCCCACTGTGAAAAAGGATAGAG	1117
Db	132	GCGAGCCCTGTGAGAGACCCCTCAGAAACCCCTTGGCTTGCCCACTGTGAAAAAGGATAGAG	73
QY	1114	GTTGGGTTTCCCCCT-TTATAGATGTGACGCACTGGGTGTTACAAGTTGTATGTGG	1172
Db	72	GTTGGGTTTCCCMCTTATATAGATGTGACGCACTGGGTGTTAAAAAGTTGTATGTGG	13
QY	1173	CATGATATCTTT	1184
Db	12	CATGATATMADT	1

[illegible]

FEATURES	Location/Qualifiers
source	1. .1023

## ORIGIN

Query Match	71.9%	Score 952;	DB 9;	Length 1023;
Best Local Similarity	98.9%	Pred. No. 1.9e-187;		
Matches 963; Conservative	5;	Mismatches 5;	Indels 1;	Gaps 1.

OY      8 GGCTTGACCTTCTCTCTTAAAGCGCGCCGAGGACCCCATGCGCCGAGTCCCGACACTCG 67

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Db 51 GATCTGCTCTTGGCTTTTAAAGCGGCGCCGAGAGCCATGCGCGGACCTCG 110
Qy 68 GGGAGGAGTCAACGACCAACCGGCTGTGGGCTGGAGAGTTCCGTATTTGG 127
Db 111 GGGAGGAGTCAACGACCAACCGGCTGTGGGCTGGAGAGTTCCGTATTTGG 170
Qy 128 ACGAGAGCAGACCGCTGCTGCTGCTTAAACATGAGATTAAGATAGTTACAGTTAC 187
Db 171 ACGAGAGCAGACCGCTGCTGCTGCTTAAACATGAGATTAAGATAGTTACAGTTAC 230
Qy 188 GGGTCTCTTGGCTGTGGGAGAGCTGTCTTGGGAGGCTTATGACCCCAACCATAG 247
Db 221 GGGTCTCTTGGCTGTGGGAGAGCTGTCTTGGGAGGCTTATGACCCCAACCATAG 290
Qy 248 GCCCAAGCTGTGCTATCATGTGAGAGCTTACCTGATGAGATACCATCTCTAG 307
Db 291 GCCCAAGCTGTGCTATCATGTGAGAGCTTACCTGATGAGATACCATCTCTAG 350
Qy 308 ACTCAGTTTCTGCGCTTGTGTACCAATCAAGATTGACGGCGTGGAGCATGCTTC 367
Db 351 ACTCAGTTTCTGCGCTTGTGTACCAATCAAGATTGAGCGGTGGAGCATGCTTC 410
Qy 368 TCGAGCTCTGCGAGATGATGATGTATGTCTTGGAGACCTGTCTCTTTCACCCCA 427
Db 411 TCGAGCTCTGCGAGATGATGATGTATGTCTTGGAGACCTGTCTCTTTCACCCCA 470
Qy 428 GGGGCTGAGCCCTGGCAGCTTCAATGGGAGATGTGTCTTGTTCACCTTCTGTTACT 487
Db 471 GGGGCTGAGCCCTGGCAGCTTCAATGGGAGATGTGTCTTGTTCACCTTCTGTTACT 530
Qy 488 ATGCTGTGTCTTCTCCACACGCTGGGCTGTGGAGAAATGAGACAGACAGATGAGC 547
Db 531 ATGCTGTGTCTTCTCCACACGCTGGGCTGTGGAGAAATGAGACAGACAGATGAGC 590
Qy 548 TCTACCAAGGCTGTGAGAGCTGTGCTGTAGCCCACTGTGCTGCTTACCACTACT 607
Db 591 TCTACCAAGGCTGTGAGAGCTGTGCTGTAGCCCACTGTGCTGCTTACCACTACT 650
Qy 608 CCTGCAAGAGAGATTTCAATTTGGAGAGCTTTCACAGTCCCAAGCTATACCTGTGCC 667
Db 651 CCTGCAAGAGAGATTTCAATTTGGAGAGCTTTCACAGTCCCAAGCTATACCTGTGCC 710
Qy 668 TCGGCTTTTCTAGCTGATGATGTCTTTCAGCTCTTTCCTGCTTCTGCTTCA 727
Db 711 TCGGCTTTTCTAGCTGATGATGTCTTTCAGCTCTTTCCTGCTTCTGCTTCA 770
Qy 728 GCACTAGTATTTCAATGTGACACACCACTCAGCTCCGTGAACCTTGTGAACACAGCCGA 787
Db 771 GCACTAGTATTTCAATGTGACACACCACTCAGCTCCGTGAACCTTGTGAACACAGCCGA 830
Qy 788 TTTACCTTGAAGAGACCTTCTGAACACCTTGTGACAGATGTCTCAATGTGCTTACGCTTGC 847
Db 831 TTTACCTTGAAGAGACCTTCTGAACACCTTGTGACAGATGTCTCAATGTGCTTACGCTTGC 890
Qy 848 ATGTAAACAGCGCTGCAAAACGCTGCTGCGGTAAACAGCGCTGAAAAGCGCTGCGC 907
Db 891 ATGTAAACAGCGCTGCAAAACGCTGCTGCGGTAAACAGCGCTGAAAAGCGCTGCGC 949
Qy 908 GTAAACAGCGCTGCAAAACGCTGCTGCGCAACAGATTCAAGTGTGAGCTCAAGAAAGGC 967
Db 950 GTAAACAGCGCTGCAAAACGCTGCTGCGCAACAGATTCAAGTGTGAGCTCAAGAAAGGC 1009
Qy 968 CTGAAAGAGAGCCT 981
Db 1010 CTGAAAGAGAGCCTT 1023

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RESULT 3
LOCUS BX421512 1201 bp mRNA linear EST 15-MAY-2003
DEFINITION BX421512 Homo sapiens B CELLS (RAMOS CELL LINE) Homo sapiens cDNA
clone CS00G007YM24 5-PRIME, mRNA sequence.
ACCESSION BX421512

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VERSION BX421512.1 GI:30769692
KEYWORDS EST
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
TITLE 1 (bases 1 to 1201)
JOURNAL Li W.B., Gruber C., Jessee J., and Poyas D.
FULL-LENGTH cDNA libraries and normalization
COMMENT Unpublished (2001)
CONTACT: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7413.r
Contact : Feng Liang Email : fliang@life.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS00G007BG12QPl.
FEATURES
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location/Qualifiers
1..1201
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/clone="CS00G007YM24"
/issue_type="B CELLS (RAMOS CELL LINE)"
/cell_line="RAMOS CELL LINE"
/clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE)"
/notes="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

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## ORIGIN

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Query Match 71.1%; Score 941.4; DB 13; Length 1201;
Best Local Similarity 98.5%; Pred. No. 3e-185;
Matches 976; Conservative 5; Mismatches 6; Indels 4; Gaps 3;
Qy 6 GAGGCTGTGCTCTTGTCTTAAAGCGGCGGAGAGCCCATGCGCGAGTCCGACACT 65
Db 55 GGGATTTCTGCTCTTGTCTTAAAGCGGCGGAGAGCCCATGCGCGAGTCCGACACT 114
Qy 66 CGGAGGAGCAGTCAACCGACCAACCGGAGCGCTGTGGGCTGGAGAGTTCTGTATTT 125
Db 115 CGGAGGAGCAGTCAACCGACCAACCGGAGCGCTGTGGGCTGGAGAGTTCTGTATTT 174
Qy 126 GAGCAGAGAGAGACGCGCTGCTGCTTAAACATCGAGATTAAGATAGGTTACAGTT 185
Db 175 GAGCAGAGAGAGACGCGCTGCTGCTTAAACATCGAGATTAAGATAGGTTACAGTT 234
Qy 186 ACGGCTGTCTTGTGCGTGGGAGAGAGTGTCTTGGGAGGAGCTATGACCCCAACGAT 245
Db 235 ACGGCTGTCTTGTGCGTGGGAGAGAGTGTCTTGGGAGGAGCTATGACCCCAACGAT 294
Qy 246 AGGCCAAGCCTGCTGCTTATCATGTGAGCACTTACCTCTATGAGATACCATCTCTC 305
Db 295 AGGCCAAGCCTGCTGCTTATCATGTGAGCACTTACCTCTATGAGATACCATCTCTC 354
Qy 306 AGACTCAGTTTCTGCGCTTATGATGACCAATCAAGATTGACGCGGTGAGAGATGCT 365
Db 355 AGACTCAGTTTCTGCGCTTATGATGACCAATCAAGATTGACGCGGTGAGAGATGCT 414
Qy 366 TCTGAGCTGTGCCAGATGACTGATGTATGTCTTGGAGAGACCTGTCTCTTCAACC 425
Db 415 TCTGAGCTGTGCCAGATGACTGATGTATGTCTTGGAGAGACCTGTCTCTTCAACC 474
Qy 426 CAGGCGCTGAGCTGCGCAGCTCAATGAGGAGATGTGTCTTGTCACTTCACTTGA 485
Db 475 CAGGCGCTGAGCTGCGCAGCTCAATGAGGAGATGTGTCTTGTCACTTGTGTTA 534
Qy 486 CTATGCTGTGTCTTCTCCACACGCTGCGGTGTGGAGATGAGACAGAGAGATGA 545

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QY 904 GCCCGTAAACAGCCCTGCAAAAGCTGCTGCCACACAGTTCACTGCG-AGCTCAAGGA 962  
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| | | | |  
QY 963 AA--GGCTGAAAGAGCCCTTATCTGTGCT 991  
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Db 956 AAGGGCTGGAAAGGAGCCCTTATCTGTGCT 986  
| | | | |  
RESULT 5  
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LOCUS BQ061021 1031 bp mRNA linear EST 02-APR-2002  
DEFINITION AGENCOURT\_6863016 NIH\_MGC\_99 Homo sapiens cDNA clone IMAGE:5920041  
5', mRNA sequence.  
ACCESSION BQ061021  
VERSION BQ061021.1 GI:19884692  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1031)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Lou Staudt  
cDNA Library Preparation: Rubin Laboratory  
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: L1CM2083 row: b column: 10  
High quality sequence scop: 670.  
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/tissue\_type="lymphoma, cell line"  
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/clone\_lib="NIH\_MGC\_99"  
/note="Organ: Lymph; Vector: pOTB7, Site\_1: XhoI; Site\_2:  
EcoRI; cDNA made by oligo-dT priming. Directionally cloned  
into EcoRI/XhoI sites using the following 5' adaptor:  
GGCAGGAG(G). Size-selected >500bp for average insert size  
1.8kb. Library constructed by Ling Hong in the laboratory  
of Gerald M. Rubin (University of California, Berkeley)  
using ZAP-cDNA synthesis kit (Stratagene) and Superscript  
II RT (Life Technologies). Note: this is a NIH\_MGC  
Library."

ORIGIN  
Query Match 68.4%; Score 905.4; DB 13; Length 1031;  
Best Local Similarity 98.8%; Pred. No. 9.2e-178;  
Matches 912; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Db 181 AAGAGTCTCTGGGGAAGCCTATGACCCCAACCAATGAGCCCAAGCTGCTCTAT 240  
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QY 267 CATGTGAGAGCTCTACCTGATGACATGATACGATCTCTACAGTCTGAGCTTTGCGCTT 326  
| | | | |  
Db 241 CATGTGAGAGCTCTACCTGATGACATGATACGATCTCTACAGTCTGAGCTTTGCGCTT 300  
| | | | |  
QY 327 AGTGTACCAATCAAGATTGACGGGTGAGAGCAATGCTTCCGAGCTGCTGCCAGATGA 386  
| | | | |  
Db 301 AGTGTACCAATCAAGATTGACGGGTGAGAGCAATGCTTCCGAGCTGCTGCCAGATGA 360  
| | | | |  
QY 387 CTGATGTATGCTTTGGCAGACCTGTCTCTTTCACCCAGGAGCTGAGCTGCCAGC 446  
| | | | |  
Db 361 CTGATGTATGCTTTGGCAGACCTGTCTCTTTCACCCAGGAGCTGAGCTGCCAGC 420  
| | | | |  
QY 447 CTACATGAGGATGTTGTTGTTCTGTTTCACTTGCTTACTATGCTGTGTTCTTCAC 506  
| | | | |  
Db 421 CTACATGAGGATGTTGTTGTTCTGTTTCACTTGCTTACTATGCTGTGTTCTTCAC 480  
| | | | |  
QY 507 CACGCTGGGCTTGGGAGGATGACAGACAGAGATGAGCTTACCCAGGAGCTGCCAGC 566  
| | | | |  
Db 481 CACGCTGGGCTTGGGAGGATGACAGACAGAGATGAGCTTACCCAGGAGCTGCCAGC 540  
| | | | |  
QY 567 ACTGCTGTAGCCCACTCTGCTGCTTACCACTACCACTCTGCAAGAGATTTCCA 626  
| | | | |  
Db 541 ACTGCTGTAGCCCACTCTGCTGCTTACCACTACCACTCTGCAAGAGATTTCCA 600  
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QY 627 TTGGCAGAGCTTCTTCAGGCTGCCAGCTTATACCTGTGCTGCTTTCTCAGCTGGA 686  
| | | | |  
Db 601 TTGGCAGAGCTTCTTCAGGCTGCCAGCTTATACCTGTGCTGCTTTCTCAGCTGGA 660  
| | | | |  
QY 687 TGAATGTTTAAAGCTCTTTTGTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCT 746  
| | | | |  
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QY 747 CACACCCCACTGAGCTCTGCTGCTTGTGAGAGACAGAGGATTCACCTGACAGAGCTC 806  
| | | | |  
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QY 807 TGAACCTTGAACCAAGTGTCTACATGATGCTTACGCTGATGTAACAGGCTTGCAAA 866  
| | | | |  
Db 781 TGAACCTTGAACCAAGTGTCTACATGATGCTTACGCTGATGTAACAGGCTTGCAAA 840  
| | | | |  
QY 867 GCGTGCCTGCGGTAACACAGCTGCAAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 926  
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Db 841 GCGTGCCTGCGGTAACACAGCTGCAAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900  
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QY 927 CTGCTGCCCAACAGGTTTCAAG 949  
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Db 901 CTGCTGCCCAACAGGTTTCCG 923  
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RESULT 6  
BQ062796 985 bp mRNA linear EST 02-APR-2002  
LOCUS BQ062796  
DEFINITION AGENCOURT\_6826945 NIH\_MGC\_99 Homo sapiens cDNA clone IMAGE:5924324  
5', mRNA sequence.  
ACCESSION BQ062796  
VERSION BQ062796.1 GI:19889936  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 985)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Lou Staudt  
cDNA Library Preparation: Rubin Laboratory  
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LNCM2094 row: d column: 21  
 High quality sequence stop: 744.  
 Location/Qualifiers

## FEATURES

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/note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dt priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

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## ORIGIN

Query Match 68.2%; Score 903; DB 13; Length 985;  
 Best Local Similarity 97.6%; Pred. No. 2.9e-177;

Matches 959; Conservative 0; Mismatches 20; Indels 4; Gaps 4;

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QY 4 GAGAGGCTCTGGCTCTTCTTAAAGCGGCCGAGAGCCATGCGAGTGGCCGACA 63
Db 2 GAGAAAGCTCTGGCTCTTCTTAAAGCGGCCGAGAGCCATGCGAGTGGCCGACA 61
QY 64 CTGGGGAGGAGGACACCGACCAACCGGACCTGTGGCTTGGAGAAAGTTGTGTAT 123
Db 62 CTGGGGAGGAGGACACCGACCAACCGGACCTGTGGCTTGGAGAAAGTTGTGTAT 121
QY 124 TTGGAGCAGAAAGCAGCAGCTGGCTGCTTAAACATCGAGATTAAGATAGTTACAG 183
Db 122 TTGGAGCAGAAAGCAGCAGCTGGCTGCTTAAACATCGAGATTAAGATAGTTACAG 181
QY 184 TTACGGGTCTCTTGGCTGGGAAAGCGTCTCTGGGAGGCTTATGACCCCAACAG 243
Db 182 TTACGGGTCTCTTGGCTGGGAAAGCGTCTCTGGGAGGCTTATGACCCCAACAG 241
QY 244 ATAGGCCCAAGCCGCTGCTATATGAGAGAGCTTAACTGATGACATACCATCC 303
Db 242 ATAGGCCCAAGCCGCTGCTATATGAGAGAGCTTAACTGATGACATACCATCC 301
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QY 364 CTTTTCAGAGCTGCTGCCAGATGACTGATGTATGCTTGGACAGCCTGTCTCTTAC 423
Db 362 CTTTTCAGAGCTGCTGCCAGATGACTGATGTATGCTTGGACAGCCTGTCTCTTAC 421
QY 424 CCCAGGGGCTGAGCTGGGCAAGCTTAAATGGGAGATTTGTGTTCTGTTCACTTCGTT 483
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QY 544 GAGCTTACCCAGGGCTTGGAGAGCTGCTGTAGAGCCACTGTGCTGCTTATGACTAC 603
Db 542 GAGCTTACCCAGGGCTTGGAGAGCTGCTGTAGAGCCACTGTGCTGCTTATGACTAC 601
QY 604 CACTCTGCAAGAGAGATTCATTTGGAGAGCTTCTTCCAGGTGCCAGCTATACCTG 663
Db 602 CACTCTGCAAGAGAGATTCATTTGGAGAGCTTCTTCCAGGTGCCAGCTATACCTG 661

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QY 664 TGCTCTGGCTTTTCTCAGCTGATGATGTCTTCAAGCTCTTTCTGTCTGTCCCT 723
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QY 724 CACGACCTGATTTTATCATATGACACCCACCTCAGTCCGTGAACCTTGGAGAACAG 783
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QY 903 TG-CCGTTAAACACGCTTGAACCGCTGCTG-CCGACAGGTTACAGT-GCAGCTCAA 959
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QY 960 GAAAGGCTGAAAGAGCCCTT 982
Db 962 GAAAGGCTGAAAGAGCCCT 984

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RESULT 7
BQ065603
LOCUS
DEFINITION
BQ065603 986 bp mRNA linear EST 02-APR-2002
AGENCOURT 6875295 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5930157
5', mRNA sequence.
BQ065603.1 GI:19894649
EST.
KEYWORDS
BQ065603.1 GI:19894649
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 986)
NIH-MGC http://mgc.mci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LNCM2109 row: g column: 22
High quality sequence stop: 654.
Location/Qualifiers
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/mol_type="mRNA"
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_99"
/note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dt priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

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## FEATURES

source

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/clone_lib="NIH_MGC_99"
/note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dt priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

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## ORIGIN



Query Match 67.2%; Score 889.8; DB 13; Length 986;  
 Best Local Similarity 96.8%; Pred. No. 1.6e-174;  
 Matches 952; Conservative 0; Mismatches 22; Indels 9; Gaps 4;

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QY 12 CTGGCTCTTGTCTTTAGGCGGCGCCGAGAGAGCCCATGCGCGAGTCCCGACACTCGGGGA 71
DB 1 CTGGCTCTTGTCTTTAGGCGGCGCCGAGAGAGCCCATGCGCGAGTCCCGACACTCGGGGA 60
QY 72 GGCACATCCAGACACACCCGAGACCGGCTGTGGGCGTGGGAGAGTTCGTATATTGGACGA 131
DB 61 GGCACATCCAGACACACCCGAGACCGGCTGTGGGCGTGGGAGAGTTCGTATATTGGACGA 120
QY 132 GAAGAGAGACGCGCTGCTGCTCCCTTAACATCGAGATTAAGATAGATTACAGTTACGAGT 191
DB 121 GAAGAGAGACGCGCTGCTGCTCCCTTAACATCGAGATTAAGATAGATTACAGTTACGAGT 180
QY 192 GCTCTTGGCTGGGAGAGAGTGTCTGTGGGAGGCGCTATGACCCCGACCCAGATAGGCC 251
DB 181 GCTCTTGGCTGGGAGAGAGTGTCTGTGGGAGGCGCTATGACCCCGACCCAGATAGGCC 240
QY 252 AAGCGTGTGCGCTATCATGTGGGAGGCTTACCTGTATGAGACATACCGATCCTCAGACTC 311
DB 241 AAGCGTGTGCGCTATCATGTGGGAGGCTTACCTGTATGAGACATACCGATCCTCAGACTC 300
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QY 372 GCTGTGTCCAGATGACTGATGATGATGCTTGGCAGACACTGTCTCTTTCACCCGAGGC 431
DB 361 GCTGTGTCCAGATGACTGATGATGATGCTTGGCAGACACTGTCTCTTTCACCCGAGGC 420
QY 432 CTGACCTGTGCGACGCTTACATAGGGAGATGTGTCTTCTGTTCACTTGTCTTACTATGTC 491
DB 421 CTGACCTGTGCGACGCTTACATAGGGAGATGTGTCTTCTGTTCACTTGTCTTACTATGTC 480
QY 492 CTGTCTCTTCTCCACACGCTGTGGGCTGTGGAGAGATGAGACAGACAGAGATGAGTCTA 551
DB 481 CTGTCTCTTCTCCACACGCTGTGGGCTGTGGAGAGATGAGACAGACAGAGATGAGTCTA 540
QY 552 CCGAGGCGCTGAGAGACCTGCTGTAGCCCACTGTGCTGCTTGTAGCACTACACTCTG 611
DB 541 CCGAGGCGCTGAGAGACCTGCTGTAGCCCACTGTGCTGCTTGTAGCACTACACTCTG 600
QY 612 CCAAGAGAGATTCATTGGAGAGCTTCTTCCAGGTGCCAGCTTATACCTGTGCTGCG 671
DB 601 CCAAGAGAGATTCATTGGAGAGCTTCTTCCAGGTGCCAGCTTATACCTGTGCTGCG 660
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QY 792 CCTGAGCAGAGACTTGTGAACCTCTGAGCAGTGTCTTCACTAGTGTCTACGCTTGTGAT 851
DB 781 CCTGAGCAGAGACTTGTGAACCTCTGAGCAGTGTCTTCACTAGTGTCTACGCTTGTGAT 840
QY 852 AAACAGCGCTGCAAAAGCGTG--CTGCGGCTTAAACAGCGCTGCAAAAGCGTGCT--GGCC 907
DB 841 AAACAGCGCTGCAAAAGCGTG--CTGCGGCTTAAACAGCGCTGCAAAAGCGTGCT--GGCC 900
QY 908 GTAAACAGCGCTGCAAAAGCGTGCT--TGCACACAGGTTTCACTGACGCTCAAG--A 962
DB 901 ATAAACAGCGCTGCAAAAGCGTGCTGCGCCCAACAGGTTTCACTGACGCTCAAGGGA 960
QY 963 AAGGCTGAAAGAGAGCCCTTATC 985
DB 961 AAGGCTGAAAGAGAGCCCTTATC 983

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RESULT 8
B0061232
LOCUS B0061232 1029 bp mRNA linear EST 02-APR-2002
DEFINITION AGENCOURT 6863247 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5920271
5', mRNA sequence.
ACCESSION B0061232
VERSION B0061232.1 GI:19885088
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 1029)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM2083 row: k column: 24
High quality sequence drop: 728.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5920271"
/issue_type="Lymphoma, cell line"
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/note="Organ: Lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
library."
ORIGIN
Query Match 67.0%; Score 886.6; DB 13; Length 1029;
Best Local Similarity 97.0%; Pred. No. 7.4e-174;
Matches 947; Conservative 0; Mismatches 20; Indels 9; Gaps 4;
QY 20 TGCCTTAAAGCGGCGGAGAGAGCCATGAGCCGAGTCCCGACACTCGGGAGGAGTCA 79
DB 1 TGCCTTAAAGCGGCGGAGAGAGCCATGAGCCGAGTCCCGACACTCGGGAGGAGTCA 60
QY 80 CCGACACCCGAGACCGCTGTGGGCTGTGGAGAACTTGTGATTTTGAACGAGAGCAGC 139
DB 61 CCGACACCCGAGACCGCTGTGGGCTGTGGAGAACTTGTGATTTTGAACGAGAGCAGC 120
QY 140 ACGCTGAGCGCTCTTAACATCGAGATTAAGATAGATTACAGTTACGGGTGCTTGC 199
DB 121 ACGCTGAGCGCTCTTAACATCGAGATTAAGATAGATTACAGTTACGGGTGCTTGC 180
QY 200 GTGCGGAGAGCGTGTCTGTGGGAGGCTTATGACCCCAACCGAGTAAAGAGCTTGC 259
DB 181 GTGCGGAGAGCGTGTCTGTGGGAGGCTTATGACCCCAACCGAGTAAAGAGCTTGC 240
QY 260 TGCCTATATGATGAGAGCTTACCTGTATGAGACGATACCGATCTCAGACTCATTCT 319
DB 241 TGCCTATATGATGAGAGCTTACCTGTATGAGACGATACCGATCTCAGACTCATTCT 300
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Db	301	GGGGCTTAGTGAACCAATCAATGAAGTTACGGCGCGGAGAGACATGCTTCTGAGCTGCTGC	360
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Db	361	CAATAGACTAT-----GTCCTGGCAGACACCTGTCTCTTTCAACCCAGAGGCGTGAGCCT	415
QY	440	GGCAGAGCTCAATAGGGAGATGTTGTGTTCTGTTTCACTCTCGTTTACTAGCTGTGTCT	499
Db	416	GGCAGAGCTCAATGGGAGATGTTGTGTTCTGTTTCACTCTCGTTTACTAGCTGTGTCT	475
QY	500	TCTTCACCAACGCTGGGGCTCTGGAGAGAAATGAGACAGACAGATGAGCTTACCCAGGC	559
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QY	560	CTGACAGAACCTGCGCTGTGAGCCACTCTGCTGCGCTTAAAGCACTACCACTCTGCCAAGAG	619
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QY	620	GATTCCATTGGCAGAGCTTCTTCCAGAGTCCAGACTATACCTGTGCGCTTCTTC	679
Db	596	GATTCCATTGGCAGAGCTTCTTCCAGAGTCCAGACTATACCTGTGCGCTTCTTC	655
QY	680	AGCTGATATGATGCTCTTTCAGGCTCTTTCGTCTCTGCTCTGCTCAACAGACTAGTATT	739
Db	656	AGCTGATATGATGCTCTTTCAGGCTCTTTCGTCTCTGCTCTGCTCAACAGACTAGTATT	715
QY	740	CATGTTGCACACCCACTCAGCTACGCTCGTGAACCTGTGAGAAACAGCGGATTTCACCTGAGCA	799
Db	716	CATGTTGCACACCCACTCAGCTACGCTCGTGAACCTGTGAGAAACAGCGGATTTCACCTGAGCA	775
QY	800	GGACCTCTGAAAACCTGTGACACAGTGTGTCAATGTGTGTAAGCCCTGATGTAAACAGCG	859
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QY	860	CTGCAAAACGCTGCGCTGCGGATTAACACGCGCTGCAAAACGCTG--CTTGCCCGTAAACAGCGC	918
Db	836	CCTGCACACGCTGCGCTGCGGATTAACACGCGCTGCAAAACGCTGCGCTGCGGATTAACAGCGC	895
QY	919	TGCAAAACGCT-GCCTGCCCAACAGATTCACGCTGC--AGCTCAAGAAAAGGCTGAAAAG	975
Db	896	TGCAAAACGCTGCGCTGCGGATTAACACGCGCTGCAAAACGCTGCGCTGCGGATTAACAGCGC	955
QY	976	AGCCCTTATCTGTGCT 991	
Db	956	GAGCCCTTATCTGTGCT 971	
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LOCUS			linear
DEFINITION	AGENCOURT_6940585 NIH_MGC_99 Homo sapiens	CDNA clone	IMAGE:5809091
ACCESSION	B0056675		
VERSION	B0056675.1	GI:19816015	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 982)		
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/.		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Robert Strusberg, Ph.D.		
	Email: rgs@nci.nih.gov		
	Tissue Procurement: Lou Staudt		
	CDNA Library Preparation: Rubin Laboratory		
	DNA Sequencing by: Agencourt Bioscience Corporation		
	found through the I.M.A.G.E. Consortium/LLNL at:		
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ORIGIN		
Query Match	66.6%; Score 881.4; DB 13; Length 982;	
Best Local Similarity	96.8%; Pred. No. 8.9e-173;	
Matches 910; Conservative	0; Mismatches 27; Indels 3; Gaps 1;	
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QY	226 CCTATGACCCCAACCCAGATAGGCCCAAGCTGCTGCTATCATGTGGCAGCTTACCT	285
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QY	346 GACGCGGTGAGGACATGCTCTTCGAGCTGCTGCAGATGATCATATGATGATGATGCA	405
Db	223 GACGCGGTGAGGACATGCTCTTCGAGCTGCTGCAGATGATCATATGATGATGATGCA	282
QY	406 GCACCTGCTCTCTTTCAACCCCAAGGCTGAGCTGCGCAGCTTCAATGGGATGTTGTG	465
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QY	466 TTTCTGTTCACTCTGTTTACTATGCTGTGTCTTCCACACAGCTGGGGTCTGGAGG	525
Db	343 TTTCTGTTCACTCTGTTTACTATGCTGTGTCTTCCACACAGCTGGGGTCTGGAGG	402
QY	526 AATGACACACAGAGATGAGCTCTTACCCAGGGCTTGCAGAGACTGCTGTAAGCCCATC	585
Db	403 AATGACACACAGAGATGAGCTCTTACCCAGGGCTTGCAGAGACTGCTGTAAGCCCATC	462
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Db	463 TGCTGCGCTTACGATCCACTCTCTGCGAAGAGAGATTCAATTTGGCAGACTTTTCCA	522
QY	646 GGTGCGCAGCTTATACCTGCTCTGCTGCTTTTTCAGGTGATGATGATGATGATGATG	705
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QY	706 TCTGTCCCTTCTGCTCCTCAAGACACTAGTATTTCAATGTTGACACACCACTACGCTCGT	765
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Db	643 GAACCTGTGGAACACAGCCGATTCACCTGAGAGAGAACCTCTGAACCTCTGAACCACTGG	702
QY	826 TCTCAATGCTGCTAGCGCTGATGTAACACGCTGCAAAAGCTGCTGCGGTAAACA	885
Db	703 TCTCAATGCTGCTAGCGCTGATGTAACACGCTGCAAAAGCTGCTGCGGTAAACA	762

Oy		886	GCGCTGGCAAACGCTCGTCCGCCGTAAACAACGCCTGGAACGCTTCCTGCCCAACAGGTT	945
Dd		763	CGCCTTGCAAAACGCTCGTCCGCCGTAAACAACGCCTGGAACGCTTCCTGCCCAACAGGTT	822
Oy		946	CACGTGACAGCTCAAGAAAGGCGCTTAAGAGAGACCCTTATCTGTGCTCAGAGACTCAAGAAC	1006
Dd		823	CACGTGACAGCTCAGGGAAAGGCGCTTAAGAGAGACCCTTATCTGTGCTCAGAGACTCAAGAAC	882
Oy		1006	CTTGTGGGTGATGTGTTCACATCCCGGAGCGACGACGAGAGCCAGGCGCGGAGCCC--T	1067
Dd		883	CTCTGGGTGATGTGTTCACATCCCGGAGCGACGAGAGCCAGGCGCGGAGCCCCTGT	942
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Dd		943	GCGATGAGCCCCCTCGAAAACCTTTGGGCTGCGCACGTGTAA	982
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ACCESSION	BG754764			
VERSION	BG754764.1	GI:14065417		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Mukoyota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini, Hominiidae; Homo. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)			
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/			
TITLE	1 (bases 1 to 964)			
JOURNAL	Contact: Robert Strausberg, Ph.D.			
COMMENT	Email: cgapbs-remail.nih.gov Tissue Procurement: Louis M. Staudt, M.D., Ph.D. cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: L1CM1702 row: e column: 10 High quality sequence stop: 886. Location/Qualifiers			
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ORIGIN				
Query Match	66.3%	Score 877.8;	DB 12;	Length 964;
Best Local Similarity	96.9%;	Pred. No. 5e-172;		
Matches 927; Conservative	0;	Mismatches 27;	Indels 3;	Gaps 3.
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Dd	3	CTTGAGAGGCTCTGCTCTTGGCTTTTAGAGCGCGCCGAGAGACGCGCATGAGCGAGTGCCTG	62	
Oy	61	ACACTGGGGAGGACGATCACGACACCGGACCGCTGTGGGCTTGGAGAGATTGCTG	120	

[illegible]





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Qy 365 TTCTGAGCTGCTGCAGATGA CTGATGTATGCTTTGGCAGACCTGTCTCTTCCACC 424
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Qy 425 CCAGGCGCTGAGCCTTGGCCAGCCTTACATAGGGAGATGTGTCTTTCTGTTCACTTCTT 484
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Qy 485 ACTATGCGCTGTCTTTCTTCCACACGCTGGGCTCTGGAGGAGATGACAGACAGAGATG 544
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Qy 545 AGCTTACCCAGAGGCGCTGACAGACCTGCTGTAGCCCACTGTGCTGAGCTTATGACCTACC 604
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Db 661 GCTTGGGCTTTTCTGAGCTGATGATGTGCTTCAAGCTCTTCTGCTCCCTTCTGTCCCTC 720
Qy 725 ACAGCACTAGTATTTTCAATGTTGACACACCACTCAGCTCCGTGAACTTGTGAGAAACAGC 784
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Qy 785 CGATTCACTGAGCAGGACCTTCTGAAACCTTGGACCAAGTGTCTTCACTGTGTACGCGC 844
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RESULT 14
LOCUS BM927418 1024 bp mRNA linear EST 12-MAR-2002
DEFINITION AGENCOURT_6704874 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5796834
ACCESSION BM927418
VERSION BM927418.1 GI:19377797
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 1024)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: gsa@bld-mail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
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/lab host="DH10B (phage-resistant)"
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/notes="Organ: lymph; Vector: pOT7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
library."
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ORIGIN

Query Match 64.8%; Score 858.2; DB 12; Length 1024;  
Best Local Similarity 98.8%; Pred. No. 5.9e-168;  
Matches 874; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

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1 GAGGCTTGGCTCTTCTTCTTGAAGGCGCCGAGAGAGCCATGAGCCGAGCACT 60
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[illegible]

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	5', mRNA sequence.						

FEATURES	Location/Qualifiers
SOURCE	1. .1038

Query Match	64.7%;	Score 856.6;	DB 12;	Length 1038;
Best Local Similarity	98.2%;	Pred. No. 1.3e-167;		
Matches 910; Conservative	0;	Mismatches 9;	Indels 8;	Gaps 4

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Qy	61	ACACTGGGGAGGCACTCACCGACACCCGGACCGCTGTGAGGCTGGGAGAAATTGCTG	120
Db	63	ACACTGGGGAGGCACTCACCGACACCCGGACCGCTGTGAGGCTGGGAGAAATTGCTG	122
Qy	121	TATTTGGAGGAAAGACACGCTGGGCTGCGCTTAACCATCGAGATTAAAGATAGTTA	180
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Qy	181	CAGTTACGGGTGCTCTTGGCTCGGGAGACGTGCTCTGGGAGAGGCTATGACCCCAACC	240
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QY      481 GTTTACTATGCTCTGTGTCTTCTTCCACACAGCTGGGGTCTGGAGGAATGGACACAGACAG 540
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Db      658 CTGAGGCTCTGCGCTTTCTCAGCTGATATATGCTCTTACGCTCTTCTGTGCTCTCTGATC 717
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Job time : 3773 secs

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Db      901 CTTGCGCGTAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
Qy      961 GAAAGGCTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
Db      961 GAAAGGCTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
Qy      1021 CCAATCCCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
Db      1021 CCAATCCCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
Qy      1081 CCGTGGCTTGGCCACGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
Db      1081 CCGTGGCTTGGCCACGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
```

```
Db      1081 CCGTGGCTTGGCCACGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
Qy      1141 CACGACCTGGGAGGTTTACAAAGTTGATGAGGATGAATCTTTTGTATGATTA 1200
Db      1141 CACGACCTGGGAGGTTTACAAAGTTGATGAGGATGAATCTTTTGTATGATTA 1200
Qy      1201 AATGCAAGATAGTTTATCTACTTCTGCGCAATCAGCTTCTATCTTTGACT 1260
Db      1201 AATGCAAGATAGTTTATCTACTTCTGCGCAATCAGCTTCTATCTTTGACT 1260
Qy      1261 GTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
Db      1261 GTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
Qy      1321 AAAA 1324
Db      1321 AAAA 1324

RESULT 2
PCT-US95-13663-1
; Sequence 1, Application PC/TUS9513663
; GENERAL INFORMATION:
; APPLICANT: Russo et al
; TITLE OF INVENTION: TCL-1 Gene and Protein and Related
; TITLE OF INVENTION: Methods and Compositions
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13663
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 6754-027
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 790-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEO ID NO: 1
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1324 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 49..387
PCT-US95-13663-1

Query Match      100.0%; Score 1324; DB 5; Length 1324;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1324; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```





```

OY 754 ACTCAGCTCCGTGAACCTTGTGAGAAACACAGCCGATTCACCTGAGCAGACCTCTGAAACC 813
DB 4086 ACTCAGCTCCGTGAACCTTGTGAGAAACACAGCCGATTCACCTGAGCAGACCTCTGAAACC 4145
OY 814 CTGACACAGTGTCTCAGATGTGTCTACGCTGATGTAACACGCTGCAACGCTGACC 873
DB 4146 CTGACACAGTGTCTCAGATGTGTCTACGCTGATGTAACACGCTGCAACGCTGACC 4205
OY 874 TGCCCGTAAACACGCTGCAAC-CGTGCTGCTCCCTGTAACACGCTGCAACGCTGCT 932
DB 4206 TGCCCGTAAACACGCTGCAAC-CGTGCTGCTCCCTGTAACACGCTGCAACGCTGCT 4265
OY 933 GCCCAGCAGGTTCACTGACCTCAGAGAAAGCCCTGAAAGAGCCCTTATCTGTGCTC 992
DB 4266 GCCCAGCAGGTTCACTGACCTCAGAGAAAGCCCTGAAAGAGCCCTTATCTGTGCTC 4325
OY 993 AGGACTCAGAAAGCTCTGGGTCAGTGTCTCAGATCCCGGAGCGACAGAGAGCCAGGCC 1052
DB 4326 AGGACTCAGAAAGCTCTGGGTCAGTGTCTCAGATCCCGGAGCGACAGAGAGCCAGGCC 4385
OY 1053 GCGGAGCCCTGTGATGAGACCTCTGAGAACCTCTGGCTGCGCACTGGAAGAGGATAGA 1112
DB 4386 GCGGAGCCCTGTGATGAGACCTCTGAGAACCTCTGGCTGCGCACTGGAAGAGGATAGA 4445
OY 1113 GGTGGGTTTCCCGCC-TTTATAGATGTGACGACGACCTGGGTGTTACAAAGTTGATGTG 1171
DB 4446 GGTGGGTTTCCCGCC-TTTATAGATGTGACGACGACCTGGGTGTTACAAAGTTGATGTG 4505
OY 1172 GCATGAATACCTTTTGTATGATGATTAATATGCAAGATGTTATCTAACTGTGCGC 1231
DB 4506 GCATGAATACCTTTTGTATGATGATTAATATGCAAGATGTTATCTAACTGTGCGG 4565
OY 1232 AATCAGCTTCTATCTCTGACTTAAGATCTGTGTGAGAGAGAGTGAATAGGACGCCCA 1291
DB 4566 AATCAGCTTCTATCTCTGACTTAAGATCTGTGTGAGAGAGAGTGAATAGGACGCCCA 4625
OY 1292 AATAAATAATATTCATGGA 1311
DB 4626 AATAAATAATATTCATGGA 4645

```

```

RESULT 5
PCT-US95-13663-5
Sequence 5, Application PC/TUS9513663
GENERAL INFORMATION:
APPLICANT: Russo et al
TITLE OF INVENTION: TCL-1 Gene and Protein and Related
NUMBER OF INVENTIONS: Methods and Compositions
CORRESPONDENCE ADDRESS:
ADDRESS: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13663
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Mierock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6754-027
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 790-8864/9741
TELEX: 66141 PENNIE

```

```

; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4922 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA
PCT-US95-13663-5

```

```

Query Match      61.9%; Score 819.8; DB 5; Length 4922;
Best Local Similarity 92.8%; Pred. No. 2.8e-248;
Matches 854; Conservative 28; Mismatches 34; Indels 4; Gaps 4;

```

```

OY 396 GGTCTTGGCAGACCTGCTCTCTTACCCAGGCGCTGAGCGCCAGCCTTACAAATG 455
DB 3726 GGTCTTGGYAGACCTGCTCTCTTACCCAGGCGCTGAGCGCTGAGCCTTACAAATG 3785
OY 456 GGATGTGTGTTTCTGTTCACTTGTCTTATGATGCTGTGCTTCTCACCAGCCTGG 515
DB 3786 GGATGTGTGTTTCTGTTCACTTGTCTTATGATGCTGTGCTTCTCACCAGCCTGG 3845
OY 516 GTCTGGAGGAATGAGACAGACAGAGATGAGCTTACCCAGGCGCTGACAGACTGG-CCT 574
DB 3846 GTCTGGAGGAATGAGACAGACAGAGATGAGCTTACCCAGGCGCTGAGAGACTGTGCT 3905
OY 575 GTAGCCCACTGCTGCTGCTTACGA-CATACACTCTGCTCAGAGAGATTCATTGGCA 633
DB 3906 GTAGCCCACTGCTGCTGCTTACGA-CATACACTCTGCTCAGAGAGATTCATTGGCA 3965
OY 634 GAGCTTCTTCAAGGTCGCGCAGCTATACCTGTGCTGCTGCTTCTCAGCTGATGAT 693
DB 3966 GAGCTTCTTCAAGGTCGCGCAGCTATACCTGTGCTGCTGCTTCTCAGCTGATGAT 4025
OY 694 CTTAGCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 753
DB 4026 CTTAGCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4085
OY 754 ACTCAGCTCCGTGAACCTTGTGAGAAACACAGCCGATTCACCTGAGCAGACCTCTGAAACC 813
DB 4086 ACTCAGCTCCGTGAACCTTGTGAGAAACACAGCCGATTCACCTGAGCAGACCTCTGAAACC 4145
OY 814 CTGACACAGTGTCTCAGATGTGTCTACGCTGATGTAACACGCTGCAACGCTGACC 873
DB 4146 CTGACACAGTGTCTCAGATGTGTCTACGCTGATGTAACACGCTGCAACGCTGACC 4205
OY 874 TGCCCGTAAACACGCTGCAAC-CGTGCTGCTCCCTGTAACACGCTGCAACGCTGCT 932
DB 4206 TGCCCGTAAACACGCTGCAAC-CGTGCTGCTCCCTGTAACACGCTGCAACGCTGCT 4265
OY 933 GCCCAGCAGGTTCACTGACCTCAGAGAAAGCCCTGAAAGAGCCCTTATCTGTGCTC 992
DB 4266 GCCCAGCAGGTTCACTGACCTCAGAGAAAGCCCTGAAAGAGCCCTTATCTGTGCTC 4325
OY 993 AGGACTCAGAAAGCTCTGGGTCAGTGTCTCAGATCCCGGAGCGACAGAGAGCCAGGCC 1052
DB 4326 AGGACTCAGAAAGCTCTGGGTCAGTGTCTCAGATCCCGGAGCGACAGAGAGCCAGGCC 4385
OY 1053 GCGGAGCCCTGTGATGAGACCTCTGAGAACCTCTGGCTGCGCACTGGAAGAGGATAGA 1112
DB 4386 GCGGAGCCCTGTGATGAGACCTCTGAGAACCTCTGGCTGCGCACTGGAAGAGGATAGA 4445
OY 1113 GGTGGGTTTCCCGCC-TTTATAGATGTGACGACGACCTGGGTGTTACAAAGTTGATGTG 1171
DB 4446 GGTGGGTTTCCCGCC-TTTATAGATGTGACGACGACCTGGGTGTTACAAAGTTGATGTG 4505
OY 1172 GCATGAATACCTTTTGTATGATGATTAATATGCAAGATGTTATCTAACTGTGCGC 1231
DB 4506 GCATGAATACCTTTTGTATGATGATTAATATGCAAGATGTTATCTAACTGTGCGG 4565
OY 1232 AATCAGCTTCTATCTCTGACTTAAGATCTGTGTGAGAGAGTGAATAGGACGCCCA 1291
DB 4566 AATCAGCTTCTATCTCTGACTTAAGATCTGTGTGAGAGAGTGAATAGGACGCCCA 4625

```

QY 1292 AATAAATAATTCATGGAA 1311  
| | | | |  
Db 4626 NATAAANATATTCANGGA 4645

## RESULT 6

US-08-330-272-3  
Sequence 3, Application US/08330272  
Patent No. 5985598  
GENERAL INFORMATION:  
APPLICANT: Russo et al  
TITLE OF INVENTION: TCL-1 Gene and Protein and Related  
TITLE OF INVENTION: Methods and Compositions  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/330,272  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 6754-027  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 790-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 560 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-330-272-3

Query Match 4.9%; Score 65; DB 2; Length 560;  
Best Local Similarity 100.0%; Pred. No. 2.5e-10;  
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGAGAGGCTCTGGCTCTTGGCTTTAGGCGGCCGAGACGCGCATGGCCGAGTGCCCG 60  
| | | | |  
Db 496 CTTGAGAGGCTCTGGCTCTTGGCTTTAGGCGGCCGAGACGCGCATGGCCGAGTGCCCG 555

QY 61 AACT 65  
| | | | |  
Db 556 AACT 560

## RESULT 7

PCT-US95-13663-3  
Sequence 3, Application PC/TUS9513663  
GENERAL INFORMATION:  
APPLICANT: Russo et al  
TITLE OF INVENTION: TCL-1 Gene and Protein and Related  
TITLE OF INVENTION: Methods and Compositions  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York

COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/13663  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 6754-027  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 790-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 560 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
PCT-US95-13663-3

Query Match 4.9%; Score 65; DB 5; Length 560;  
Best Local Similarity 100.0%; Pred. No. 2.5e-10;  
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGAGAGGCTCTGGCTCTTGGCTTTAGGCGGCCGAGACGCGCATGGCCGAGTGCCCG 60  
| | | | |  
Db 496 CTTGAGAGGCTCTGGCTCTTGGCTTTAGGCGGCCGAGACGCGCATGGCCGAGTGCCCG 555

QY 61 AACT 65  
| | | | |  
Db 556 AACT 560

## RESULT 8

US-08-232-463-14  
Sequence 14, Application US/08232463  
Patent No. 5670367  
GENERAL INFORMATION:  
APPLICANT: DORNER, F.  
APPLICANT: SCHEIFLINGER, F.  
APPLICANT: FALKNER, F. G.  
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 1800 Diagonal Road, Suite 500  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22313-0299  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,463  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/935,313  
FILING DATE:  
APPLICATION NUMBER: EP 91 114 300.6  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:

```

; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: PT59PT-F18
; US-08-232-463-14

Query Match          3.7%; Score 49.2; DB 1; Length 7218;
Best Local Similarity 2.3%; Pred.No.0.00013;
Matches 9; Conservative 221; Mismatches 154; Indels 0; Gaps 0;

QY 399 CTGGCAGCAGCTGCTCTCTTACCCAGGCGCTGAGCTGGCCAGCCTACATGGGGA 458
    ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1059 CTGGCAGATYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1118
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 459 TGTGTGTTTCTGTCACCTTGTTTACTATGCTGTGCTCTCTCACCAGCTGGGTC 518
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1119 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1178
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 519 TGGGAGATGAGACAGACAGATGAGCTTACCCAGGCGCTGGAGAGCTGCTGTAG 578
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1179 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1238
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 579 CCCACTCTGCTGCTTACGACTACACTCTGCGAAGAGATTCCATTGGCAGAGCT 638
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1239 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1298
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 639 TCTTCAGAGTGCAGCTATACCTGTGCTGCTTTCTCTCAGCGATGATGCTTCA 698
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1299 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1358
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 699 GCGCTCTTCTGCTCTGCTCTGCTCAGACAGCACTAGTATGATGTGCACACCACTCA 758
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1359 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1418
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 759 GCTCCGTAAGCTGTGAGAACACA 782
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1419 YYYYYYYYYYYYYYGTACCAAA 1442
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 9
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
```

```

; OTHER INFORMATION: represent a, t, c or g
; US-09-103-840A-2

Query Match          3.2%; Score 41.8; DB 3; Length 4403765;
Best Local Similarity 53.3%; Pred.No.1.6;
Matches 88; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY 3 TGAGAGGCTCTGGCTTCTTCTTAAGGCGGCCGAGAGCGCATGGCGAGTCCGAC 62
    ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 2358757 TGCGGCTGTATCTGACGTGGGCAATCCGAGTACGCAACCGCAATGGCAG 2358698
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 63 ACTCGGAGGACAGTACACCAACACCCGACCGCTGTGGCCTTGAGAAATTGCTGTA 122
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 2358697 CCTGTGACGTGTGTGACCACTGACCGGCGCGGTGAATGGGTGCGAAGACCTCTGT 2358638
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 123 TTGGACGAGAAACAGACAGCGCTGCTGCTTCAATCGAGAT 167
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 2358637 TGACGCCGAGCAGCGGCTGCGCCGACGAGGAGATCGGCGGACAT 2358593
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 10
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
; US-09-103-840A-1

Query Match          3.2%; Score 41.8; DB 3; Length 4411529;
Best Local Similarity 53.3%; Pred.No.1.6;
Matches 88; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY 3 TGAGAGGCTCTGGCTTCTTCTTAAGGCGGCCGAGAGCGCATGGCGAGTCCGAC 62
    ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 2356523 TGCGGCTGTATCTGACGTGGGCAATCCGAGTACCGCAACCGCAATGGCAG 2356464
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 63 ACTCGGAGGACAGTACACCAACACCCGACCGCTGTGGCCTTGAGAAATTGCTGTA 122
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 2356463 CCTGTGACGTGTGTGACCACTGACCGGCGCGGTGAATGGGTGCGAAGACCTCTGT 2356404
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 123 TTGGACGAGAAACAGACAGCGCTGCTGCTTCAATCGAGAT 167
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 2356403 TGACGCCGAGCAGCGGCTGCGCCGACGAGGAGATCGGCGGACAT 2356359
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 11
US-09-007-005-17/c
; Sequence 17, Application US/09007005B
; Patent No. 6258558
; GENERAL INFORMATION:
; APPLICANT: Szoestak, Jack W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rihbe
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; FILE REFERENCE: 00786/350003
; CURRENT APPLICATION NUMBER: US/09/007,005B
; CURRENT FILING DATE: 1998-01-14
```

QY	567	ACCTGCGCTTGAAGCCACACTCTGCTGGCTTTAGACACTACACTCTCCGACAGAGAGATTC	62
Db	586	ACCCGACACCAAGCTGCTCTCCACCCCCGAGCAGCACCAGCCCTCAGCCACGACAGAAACT	52
QY	627	TTTGGCAGAGCTTCTTCCAGAGTGCCCAAGTAACTGCTGCTCGAGCTTTTCTCAGCTGGA	686
Db	526	TGAGTAGGGCCACACAGCCTCTGCACTCTCTCTCTGCTCCACACTCTGCCCAGCTGGG	467
QY	687	TGATGGTC	694
Db	466	GGAGGCTC	459



RESULT 14  
US-10-204-708-81  
Sequence 81, Application US/10204708  
Patent No. 6677731  
GENERAL INFORMATION:  
APPLICANT: OLEK, Alexander  
APPLICANT: PIEPENROCK, Christian  
APPLICANT: BERRIN, Kurt  
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication  
FILE REFERENCE: 5013.1012  
CURRENT FILING DATE: 2003-05-06  
PCT/EP01/03971  
PRIOR FILING DATE: 2001-04-06  
PRIOR APPLICATION NUMBER: DE 10019058.8  
PRIOR FILING DATE: 2000-04-06  
PRIOR APPLICATION NUMBER: DE 10019173.8  
PRIOR FILING DATE: 2000-04-07  
PRIOR APPLICATION NUMBER: DE 10032529.7  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: DE 10043826.1  
NUMBER OF SEQ ID NOS: 98  
SEQ ID NO 81  
LENGTH: 5476  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
US-10-204-708-81  
Query Match 2.7%; Score 36.4; DB 4; Length 5476;  
Best Local Similarity 50.6%; Pred. No. 1.2;  
Matches 88; Conservative 0; Mismatches 86; Indels 0; Gaps 0;  
QY 1151 GGTGTACAAGTGTATGTCGCAATGACTTTTGTGAATGATGATTAATGCAAGT 1210  
DB 85 GTTATTGAATATGTTGTTTATTGTTAGTTTTTTTATATATATATATGTTAAT 144  
QY 1211 AGTTATCTAATCTGTCGCAATGAGCTTCTATCCTTGACTTAGATTCTGCGAGAGA 1270  
DB 145 TTTTGAATTTTGTAAATGAAATTTTATTTTATTTTAAATTTGTTAATTTAAAGT 204  
QY 1271 AGTGAAATAGCAGCCCCCAATTAATAATTCATGAAAAA 1324  
DB 205 AGTAAGTTAGATTATATGTTATTTAAAAAAGAAAAA 258  
RESULT 15  
US-08-311-731A-126/C  
Sequence 126, Application US/08311731A  
Patent No. 6583266  
GENERAL INFORMATION:  
APPLICANT: SMITH, DOUGLAS  
APPLICANT: MAO, JEN-I  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES  
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LABRAE FOR  
NUMBER OF SEQUENCES: 411  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: WOJF, GREENFIELD & SACKS, P.C.  
STREET: 600 ATLANTIC AVENUE  
CITY: BOSTON  
STATE: MASSACHUSETTS  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/311,731A  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: GATES, EDWARD R.  
REGISTRATION NUMBER: 31,616  
REFERENCE/DOCKET NUMBER: C0044/7125  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/720-3500  
TELEFAX: 617/720-2441  
INFORMATION FOR SEQ ID NO: 126:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 42157 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: MYCOBACTERIUM LEPRAE  
US-08-311-731A-126  
Query Match 2.7%; Score 36.4; DB 4; Length 42157;  
Best Local Similarity 53.5%; Pred. No. 4.3;  
Matches 76; Conservative 0; Mismatches 66; Indels 0; Gaps 0;  
QY 3 TGAGAGCTCTGCTCTTCTTGAAGCGGCGCCGAGAGCCAGTGGCCGAC 62  
DB 4650 TGCCCGCTTATCTTGAAGTGGGAGTCAATCCGAGTATGTAACCGGAGATGGACAA 4591  
QY 63 ACTGGGAGGAGTCAACCAACCCGACCGCTGTGGGCTGGGAGAACTTGTGTA 122  
DB 4590 CCTGTGCAAGCTTGTCAACCAATGACCGGCTGGCGAATGGGTGCTAAGAACTCTCGT 4531  
QY 123 TTGGAGAGGAAGCAGCAGCC 144  
DB 4530 TGATGCCAGCAGCGGCTGCC 4509

Search completed: June 17, 2004, 14:14:56  
Job time : 129 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 17, 2004, 10:34:30 ; Search time 579 Seconds  
(without alignment)  
9714.360 Million cell updates/sec

Title: US-09-441-242A-1  
Perfect score: 1324  
Sequence: 1 ctctgagagcctctgctctt.....catgaaaaaaaaaaaaaa 1324

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 212409041 residues  
Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N GeneSeq\_29Jan04:\*  
1: GeneSeqn1980s:\*  
2: GeneSeqn1990s:\*  
3: GeneSeqn2000s:\*  
4: GeneSeqn2001s:\*  
5: GeneSeqn2001bs:\*  
6: GeneSeqn2002s:\*  
7: GeneSeqn2003as:\*  
8: GeneSeqn2003bs:\*  
9: GeneSeqn2003cs:\*  
10: GeneSeqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1324	100.0	1324	2	AAT18876 Human TCL
2	1324	100.0	1324	4	AAK54940 Human hae
3	1324	100.0	1324	6	ABG73183 DNA encod
4	1324	100.0	1324	6	ABG73184 DNA encod
5	1280	96.7	1368	4	AA158979 Human pol
6	1280	96.7	1368	8	ADB48961 Novel hum
7	1177	88.9	1235	4	AA160765 Human pol
8	819.4	61.9	4922	2	AAT18877 Human TCL
9	511	38.6	561	3	AA889670 Human T c
10	285	21.5	285	4	AAK54596 Human hae
11	285	21.5	285	4	AAK54743 Human hae
12	283.4	21.4	285	4	AAK54793 Human hae
13	283.4	21.4	285	4	AAK54693 Human hae
14	283	21.4	318	4	AAK54724 Human hae
15	283	21.4	318	4	AAK54566 Human hae
16	240	18.1	240	4	AAK54601 Human hae
17	235	17.0	240	4	AAK54594 Human hae
18	225	17.0	228	4	AAK54604 Human hae
19	189.8	14.3	221	4	AAK54585 Human hae
20	167.8	12.7	3716	7	ABZ09916 Human 5'
21	107.6	8.1	3716	7	ABZ10065 Haematopo
22	107.6	8.1	6716	6	ABLJ3782 Human imm
23	102	7.7	3716	7	ABZ10066 Haematopo

c	24	102	7.7	6716	6	ABLJ3783	AbJ13783 Human imm
c	25	88.6	6.7	3716	7	ABZ10211	AbZ10211 Haematopo
c	26	81.2	5.1	3716	7	ABZ10212	AbZ10212 Haematopo
c	27	74.8	5.6	520	6	ABQ51088	AbQ51088 Oligonuc1
c	28	74.8	5.6	520	6	ABQ51089	AbQ51089 Oligonuc1
c	29	67.8	5.1	520	6	ABQ51087	AbQ51087 Oligonuc1
c	30	67.8	5.1	520	6	ABQ51086	AbQ51086 Oligonuc1
c	31	65	4.9	560	2	AAT18875	AAT18875 Human TCL
c	32	65	4.9	560	2	ABG73185	ABG73185 Human ttr
c	33	62.8	4.7	1152	3	AA875822	AA875822 Nucleotid
c	34	60	4.5	60	6	ABN39452	ABN39452 Human spl
c	35	51.4	3.9	2000	7	ADA71938	ADA71938 Rice gene
c	36	50.6	3.8	6486	3	AA875823	AA875823 Nucleotid
c	37	50	3.8	50	6	ABZ03492	ABZ03492 Human leu
c	38	48.2	3.6	2000	7	ADA71938	ADA71938 Rice gene
c	39	47.2	3.6	5840	8	ACC83409	ACC83409 LBP-32 hy
c	40	42.2	3.2	906	3	AACT8162	AACT8162 Human can
c	41	42.2	3.2	1437	4	AAH37772	AAH37772 Human col
c	42	42.2	3.2	3375	6	ABQ54651	ABQ54651 Human ova
c	43	41.8	3.2	110000	4	AA199682	AA199682 Continuation (24 o
c	44	41.8	3.2	110000	4	AA199683	AA199683 Continuation (24 o
c	45	41.4	3.1	3799	6	AA816458	AA816458 Corn CDNA

## ALIGNMENTS

RESULT 1  
AAT18876  
ID AAT18876 standard; CDNA; 1324 BP.

AC AAT18876;

DT 23-AUG-1996 (first entry)

DE Human TCL-1 CDNA.

KW TCL-1; chromosome-14; leukaemia; lymphoma; gene therapy; ss.

OS Homo sapiens.

FX Key Location/Qualifiers

FT CDS 49..390

FT CDS /\*tag= a

PF 23-OCT-1995; 95WO-US013663.

PR 27-OCT-1994; 94US-00330272.

PA (UYJE-) UNIV JEFFERSON THOMAS.

PA (RAGG-) RAGGIO-ITALGENE SPA.

PI Russo G, Croce CM;

DR WPI; 1996-239444/24.

DR P-PSDB; AAR94974.

XX New TCL-1 protein and gene associated with chromosome 14 abnormalities -

PT useful to develop probe, for detection, treatment and prevention of

PT diseases such as T-cell leukaemia(s) and lymphoma(s).

PS Claim 4; Page 66-67; 105pp; English.

CC A CDNA clone (AAT18876) codes for human TCL-1 protein (AAR94974). It was

CC obt'd. from the AbL1 pre-B-cell line CDNA library by screening with probes

CC derived from the human genomic library p1 prep'd. from human placental

CC DNA. The CDNA was incorporated into vector pOR30 to allow expression in

CC Escherichia coli. A TCL-1 genomic sequence (AAT18877) has also been

CC identified. The TCL-1 gene is expressed at high levels in leukemic cells

CC carrying a t(14;14)(q11;q32) translocation or an inv(14)(q11;q32)  
CC inversion. The gene and its probes can be used for the diagnosis or  
CC treatment of conditions associated with chromosome 14 abnormalities, esp.  
CC T-cell leukemia and lymphoma

Sequence 1324 BP; 293 A; 376 C; 348 G; 307 T; 0 U; 0 Other;

Query Match	100.0%	Score 1324;	DB 2;	Length 1324;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1324; Conservative	0;	Mismatches	0;	Gaps 0

QY	CTTGAGAGGCTCGGCTCTTGGTCTTTAGAGGCGCCCGAGACCCCATGCGAGTGGCCG	60
Db	CTTGAGAGGCTCGGCTCTTGGTCTTTAGAGGCGCCCGAGACCCCATGCGAGTGGCCG	60
QY	ACACTCGGGAGGAGCACTCAACCAACCGGACCGCTGTGGGCTGGGAGAAATTGCTG	120
Db	ACACTCGGGAGGAGCACTCAACCAACCGGACCGCTGTGGGCTGGGAGAAATTGCTG	120
QY	ACACTCGGGAGGAGCACTCAACCAACCGGACCGCTGTGGGCTGGGAGAAATTGCTG	120
Db	ACACTCGGGAGGAGCACTCAACCAACCGGACCGCTGTGGGCTGGGAGAAATTGCTG	120
QY	TATTTGAGAGAGCAAGCAAGCTCTGGCTGCTTAACTCATGAGATPAAAGATAGTTA	180
Db	TATTTGAGAGAGCAAGCAAGCTCTGGCTGCTTAACTCATGAGATPAAAGATAGTTA	180
QY	CAGTTACGGAGTGTCTTGGCTGGAGAAAGCGTCGCTGGGAGAGCCCTATGACCCCAAC	240
Db	CAGTTACGGAGTGTCTTGGCTGGAGAAAGCGTCGCTGGGAGAGCCCTATGACCCCAAC	240
QY	CAGTTACGGAGTGTCTTGGCTGGAGAAAGCGTCGCTGGGAGAGCCCTATGACCCCAAC	240
Db	CAGTTACGGAGTGTCTTGGCTGGAGAAAGCGTCGCTGGGAGAGCCCTATGACCCCAAC	240
QY	CAGATPAGGCCCAAGCCTGTGCTCTATCATGTGGAGCTCTACCTGATGAGCATACCA	300
Db	CAGATPAGGCCCAAGCCTGTGCTCTATCATGTGGAGCTCTACCTGATGAGCATACCA	300
QY	TGCTCGAGTCCAGATTTCTGGGGCTTAATGTATCCATCATAGATTGACGCGGTGAGAGAC	360
Db	TGCTCGAGTCCAGATTTCTGGGGCTTAATGTATCCATCATAGATTGACGCGGTGAGAGAC	360
QY	TGCTCGAGTCCAGATTTCTGGGGCTTAATGTATCCATCATAGATTGACGCGGTGAGAGAC	360
Db	TGCTCGAGTCCAGATTTCTGGGGCTTAATGTATCCATCATAGATTGACGCGGTGAGAGAC	360
QY	ATGCTTCTGAGCTGCTGCAAGATGACTGATGTATGTGGCTGGAGAGACCTGTCTCTTT	420
Db	ATGCTTCTGAGCTGCTGCAAGATGACTGATGTATGTGGCTGGAGAGACCTGTCTCTTT	420
QY	ATGCTTCTGAGCTGCTGCAAGATGACTGATGTATGTGGCTGGAGAGACCTGTCTCTTT	420
Db	ATGCTTCTGAGCTGCTGCAAGATGACTGATGTATGTGGCTGGAGAGACCTGTCTCTTT	420
QY	ATGCTTCTGAGCTGCTGCAAGATGACTGATGTATGTGGCTGGAGAGACCTGTCTCTTT	420
Db	ATGCTTCTGAGCTGCTGCAAGATGACTGATGTATGTGGCTGGAGAGACCTGTCTCTTT	420
QY	CACCCGAGGGCTGAGCTGCGGCAAGCTTCAATATGGAGATGTGTGTTCTGTTCACTTTC	480
Db	CACCCGAGGGCTGAGCTGCGGCAAGCTTCAATATGGAGATGTGTGTTCTGTTCACTTTC	480
QY	CACCCGAGGGCTGAGCTGCGGCAAGCTTCAATATGGAGATGTGTGTTCTGTTCACTTTC	480
Db	CACCCGAGGGCTGAGCTGCGGCAAGCTTCAATATGGAGATGTGTGTTCTGTTCACTTTC	480
QY	GTTTACTATGACTGCTGATCTTCTCCACAACGCTGGGGGTCTGGAGAGATGAGACAGAG	540
Db	GTTTACTATGACTGCTGATCTTCTCCACAACGCTGGGGGTCTGGAGAGATGAGACAGAG	540
QY	GTTTACTATGACTGCTGATCTTCTCCACAACGCTGGGGGTCTGGAGAGATGAGACAGAG	540
Db	GTTTACTATGACTGCTGATCTTCTCCACAACGCTGGGGGTCTGGAGAGATGAGACAGAG	540
QY	GATGAGCTTCAACCGAGGCTGCAAGAACCTGCTGTAGCCCACTGTCTGCTTATGACAC	600
Db	GATGAGCTTCAACCGAGGCTGCAAGAACCTGCTGTAGCCCACTGTCTGCTTATGACAC	600
QY	GATGAGCTTCAACCGAGGCTGCAAGAACCTGCTGTAGCCCACTGTCTGCTTATGACAC	600
Db	GATGAGCTTCAACCGAGGCTGCAAGAACCTGCTGTAGCCCACTGTCTGCTTATGACAC	600
QY	TACCACTCTCTGCGAAGAGAGATTCAATTTGGCAGAGCTTTCTTCAGAGTGGCCAGCTATAC	660
Db	TACCACTCTCTGCGAAGAGAGATTCAATTTGGCAGAGCTTTCTTCAGAGTGGCCAGCTATAC	660
QY	TACCACTCTCTGCGAAGAGAGATTCAATTTGGCAGAGCTTTCTTCAGAGTGGCCAGCTATAC	660
Db	TACCACTCTCTGCGAAGAGAGATTCAATTTGGCAGAGCTTTCTTCAGAGTGGCCAGCTATAC	660
QY	CTGTGCTCTCGGCTTTTCTCAGCTGATGATGTATTTGAGGCTCTTCTGTGCTCTGTGC	720
Db	CTGTGCTCTCGGCTTTTCTCAGCTGATGATGTATTTGAGGCTCTTCTGTGCTCTGTGC	720
QY	CTGTGCTCTCGGCTTTTCTCAGCTGATGATGTATTTGAGGCTCTTCTGTGCTCTGTGC	720
Db	CTGTGCTCTCGGCTTTTCTCAGCTGATGATGTATTTGAGGCTCTTCTGTGCTCTGTGC	720
QY	CCTCAAGCACTAGATTTTCAATGTTGACACCACTCAGCTCGGTGAACTTGTGAGAAACA	780
Db	CCTCAAGCACTAGATTTTCAATGTTGACACCACTCAGCTCGGTGAACTTGTGAGAAACA	780
QY	CCTCAAGCACTAGATTTTCAATGTTGACACCACTCAGCTCGGTGAACTTGTGAGAAACA	780
Db	CCTCAAGCACTAGATTTTCAATGTTGACACCACTCAGCTCGGTGAACTTGTGAGAAACA	780
QY	CAGCGGATTTCACTGAGCGAGAACTCTGAAAACCTTGACCAAGTGTCCTCAATGGTGCTA	840
Db	CAGCGGATTTCACTGAGCGAGAACTCTGAAAACCTTGACCAAGTGTCCTCAATGGTGCTA	840
QY	CAGCGGATTTCACTGAGCGAGAACTCTGAAAACCTTGACCAAGTGTCCTCAATGGTGCTA	840
Db	CAGCGGATTTCACTGAGCGAGAACTCTGAAAACCTTGACCAAGTGTCCTCAATGGTGCTA	840
QY	CGCCTGCAATGTAAACAGCGCTGCAAAAGCTGCTGCGGTGAAACAGCGCTGCAAAAGCTG	900
Db	CGCCTGCAATGTAAACAGCGCTGCAAAAGCTGCTGCGGTGAAACAGCGCTGCAAAAGCTG	900
QY	CGCCTGCAATGTAAACAGCGCTGCAAAAGCTGCTGCGGTGAAACAGCGCTGCAAAAGCTG	900
Db	CGCCTGCAATGTAAACAGCGCTGCAAAAGCTGCTGCGGTGAAACAGCGCTGCAAAAGCTG	900
QY	CTGTGCGGTAAACAGCGCTGCAAAAGCTGCTGCTGCAACAGGTTCAAGTCAAGCTCAAG	960
Db	CTGTGCGGTAAACAGCGCTGCAAAAGCTGCTGCTGCAACAGGTTCAAGTCAAGCTCAAG	960

Db	901	CCCTGCCGTTAAACAGCGCTGCAAAGCGTGCCTGCCACACAGGTTTCAGCTGCAGCTCAAG	960
QY	961	GAAAGGCTTGAAAGAGGCCCTTATCTGTGTCTCAGAGCTCAGAAAGCCTCTGGGCTCAGTGGT	1020
Db	961	GAAAGGCTTGAAAGAGGCCCTTATCTGTGTCTCAGAGCTCAGAAAGCCTCTGGGCTCAGTGGT	1021
QY	1021	CCACATCCCGGGAGCCACACAGAGAGGCCAGGCCGGGAGACCCTGTGTGAATGAGGCCCTCAGAA	1080
Db	1021	CCACATCCCGGGAGCCACACAGAGAGGCCAGGCCGGGAGACCCTGTGTGAATGAGGCCCTCAGAA	1081
QY	1081	CCCTTGGCTTGGCCCGCAGTGGA AAAAGGATAGAGGTTGGGTTTCCCCCTTTATAGATGAT	1140
Db	1081	CCCTTGGCTTGGCCCGCAGTGGA AAAAGGATAGAGGTTGGGTTTCCCCCTTTATAGATGAT	1141
QY	1141	CAGCAGCTTGAGGTTTAAACAAAGTGTATGTGGCATGAATACTTTTGTATGATGTGATTA	1200
Db	1141	CAGCAGCTTGAGGTTTAAACAAAGTGTATGTGGCATGAATACTTTTGTATGATGTGATTA	1201
QY	1201	AATGCAAAATAGTTTATCTTAATCTTCGTGGCAATCAGTTCTTATTCCTTGACTTGAATTC	1260
Db	1201	AATGCAAAATAGTTTATCTTAATCTTCGTGGCAATCAGTTCTTATTCCTTGACTTGAATTC	1261
QY	1261	GGTGGAGAGAAAGTGAAATAGCAGAGCCCAATAATAAAAATATTCATGTGA AAAAAAAAAA	1320
Db	1261	GGTGGAGAGAAAGTGAAATAGCAGAGCCCAATAATAAAAATATTCATGTGA AAAAAAAAAA	1321
QY	1321	AAAAA 1324	
Db	1321	AAAAA 1324	

## RESULT 2

ID AAK54940 standard; cDNA; 1324 BP

AC AAK54940;

DT 13-NOV-2001 (first entry)

DE Human haematological malignancy-related antigen coding sequence #6665.

Human; cytostatic; vascular; gene therapy; vaccine; lymphoma;

follicular lymphoma; Hodgkin's lymphoma; non-Hodgkin's lymphoma; s

OS Homo sapiens.

PN WO200164886-A2

PD 07-SEP-2001

PF 01-MAR-2001; 2001WO-US007272.  
XX

PR 01-MAR-2000; 2000US-0186126P.  
PB 17-MAR-2000 2000US-0186470P

PR 27-APR-2000; 2000US-0200545P.  
DB 29-APR-2000; 2000US-0200303P

PR 28-APR-2000; 2000US-0200779P.  
PB 01-MAY-2000; 2000US-0200000P

PR 04-MAY-2000; 2000US-0202084P.  
PR 22-MAY-2000; 2000TS-0206301P

PR 14-JUL-2000; 2000US-0218950P.  
PR 03-AUG-2000; 2000US-0222903P

PR 04-AUG-2000; 2000US-0223416P.  
PR 07-AUG-2000; 2000US-0223378P

XX (CORT-) CORTXA CORD  
PA

XX  
PI Gaiger A Algate PA Mannion J.

XX  
DR  
WPT: 2001-514842/56

XX  
PT  
Compositions and meth











DB 1145 GCTTCCCACTGGAAGGATAGAGGTGGTTCCCTTTTATAGATGTCAGC 1204  
QY 1146 ACCTGGGTGTTCAGAAAGTTATGTGGCATGTAACTTTTGTATGATGTTAAATGC 1205  
DB 1205 ACCTGGGTGTTCAGAAAGTTATGTGGCATGTAACTTTTGTATGATGTTAAATGC 1264  
QY 1206 AAGATAGTTTATCTAAGTTCTGTGGCAATCAGCTTCTATCCTTGACTTAGATTCGTGGT 1265  
DB 1265 AAGATAGTTTATCTAAGTTCTGTGGCAATCAGCTTCTATCCTTGACTTAGATTCGTGGT 1324  
QY 1266 AGAGAGTGAAGATAGGAGCCGCCCAATTAATAATATTCATG 1309  
DB 1325 AGAGAGTGAAGATAGGAGCCGCCCAATTAATAATATTCATG 1368

RESULT 6  
ADB48961  
ID ADB48961 standard; cDNA; 1368 BP.  
XX  
AC ADB48961;  
XX  
DT 04-DEC-2003 (first entry)  
XX  
DE Novel human cDNA SEQ ID NO 871.  
XX  
KW 88; cancer; neurodegenerative disease; human.  
XX  
OS Homo sapiens.  
XX  
PN US2003104529-A1.  
XX  
PD 05-JUN-2003.  
XX  
PE 04-JAN-2002; 2002US-00037270.  
XX  
PR 21-JAN-2000; 2000US-00488725.  
XX  
PR 25-APR-2000; 2000US-00552317.  
XX  
PR 19-JUL-2000; 2000US-00620312.  
XX  
PA (ZHOU/) ZHOU P.  
PA (TANG/) TANG Y T.  
PA (LIUC/) LIU C.  
PA (ASUNDI/) ASUNDI V.  
PA (DRMANAC/) DRMANAC R T.  
PI Zhou P, Tang YT, Liu C, Asundi V, Drmanac RT;  
DR MPI, 2003-678194/64.  
XX  
PT New polynucleotide, useful for treating diseases e.g., cancer or  
XX neurodegenerative diseases.  
XX  
PS Claim 1; SEQ ID NO 871; 99pp; English.  
XX  
CC The invention relates to a polynucleotide comprising a sequence given in  
CC the specification, or its mature protein-coding portion, or its  
CC complement. The polynucleotide is useful for treating diseases e.g.,  
CC cancer or neurodegenerative diseases and many others listed in the  
CC specification. The present sequence represents a novel human cDNA. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification but was obtained in electronic format directly from USPTO  
CC at [seqdata.uspto.gov/sequence.html?DocID=20030104529](http://seqdata.uspto.gov/sequence.html?DocID=20030104529).  
XX  
SQ Sequence 1368 BP; 287 A; 395 C; 366 G; 320 T; 0 U; 0 Other;

Query Match 96.7%; Score 1280; DB 8; Length 1368;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1302; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 8 GCGCTGTGCTCTTCTTCTTACGCGCCCGAGAGACCCGATGCGCCGACACTCG 67  
DB 65 GCGCTGTGCTCTTCTTCTTACGCGCCCGAGAGACCCGATGCGCCGACACTCG 124

QY 68 GGGAGGAGTACCGACACCGACCGCGCTGTGGGCTGGGAGAGTTGCTATTTGG 127  
DB 125 GGGAGGAGTACCGACACCGACCGCGCTGTGGGCTGGGAGAGTTGCTATTTGG 184  
QY 128 ACGAGAGACAGACGCTGTGGTCCCTTAAACATGAGATTAAGATAGTTTACAGTTAC 187  
DB 185 ACGAGAGACAGACGCTGTGGTCCCTTAAACATGAGATTAAGATAGTTTACAGTTAC 244  
QY 188 GGGTCTCTTGGGCTGGGAGACGTCGTCTGGGGAGGCTTATGACCCCGACGATAG 247  
DB 245 GGGTCTCTTGGGCTGGGAGACGTCGTCTGGGGAGGCTTATGACCCCGACGATAG 304  
QY 248 GCCCAAGGCTGCTTCAATGTGGGAGCTTCAACCGATGAGATACGATCCCTAG 307  
DB 305 GCCCAAGGCTGCTTCAATGTGGGAGCTTCAACCGATGAGATACGATCCCTAG 364  
QY 308 ACTCCAGTTTCTGGCGCTTAAAGTACCAATCAAGATTGACGGCGTGGAGGACATGCTTC 367  
DB 365 ACTCCAGTTTCTGGCGCTTAAAGTACCAATCAAGATTGACGGCGTGGAGGACATGCTTC 424  
QY 368 TCGAGCTGCTGCGAGATGATGATGTATGCTTGGACAGACCTGTCTTTCACCCCA 427  
DB 425 TCGAGCTGCTGCGAGATGATGATGTATGCTTGGACAGACCTGTCTTTCACCCCA 484  
QY 428 GGGGCTGAGCCTGGGCGACGCTTCAATGGGAGATGTTGTCTGTTCACTTCGTTTACT 487  
DB 485 GGGGCTGAGCCTGGGCGACGCTTCAATGGGAGATGTTGTCTGTTCACTTCGTTTACT 544  
QY 488 ATGCTGTGTCTTCTCCACACAGCTGTGGGTCTGGAGAGATGACAGACAGAGATGAGC 547  
DB 545 ATGCTGTGTCTTCTCCACACAGCTGTGGGTCTGGAGAGATGACAGACAGAGATGAGC 604  
QY 548 TCTACCCAGGCGCTGCGAGACCTGTGTAGCCACTTGTCTGCTTACGACTACCACT 607  
DB 605 TCTACCCAGGCGCTGCGAGACCTGTGTAGCCACTTGTCTGCTTACGACTACCACT 664  
QY 608 CCTGCGAAGAGAGATTTCATTGGGAGAGCTTCCCA-GGTGCCACCTTATACCTGTGC 666  
DB 665 CCTGCGAAGAGAGATTTCATTGGGAGAGCTTCCCA-GGTGCCACCTTATACCTGTGC 724  
QY 667 CTCGGCTTTTTCAGCTGATGATGTCTTCAAGCTCTTCTGCTTCTGTCTTCTGCTCAG 726  
DB 725 CTCGGCTTTTTCAGCTGATGATGTCTTCAAGCTCTTCTGCTTCTGTCTTCTGCTCAG 784  
QY 727 AGCACTAGTATTTCATGTTCACACCACTGAGCTCGGTGAACCTTGTGAACACAGCCG 786  
DB 785 AGCACTAGTATTTCATGTTCACACCACTGAGCTCGGTGAACCTTGTGAACACAGCCG 844  
QY 787 ATTCACTGAGACAGACCTCTGMAAACCTTGAACCAAGTGTCTCANAATGTCTAGCCCTG 846  
DB 845 ATTCACTGAGACAGACCTCTGMAAACCTTGAACCAAGTGTCTCANAATGTCTAGCCCTG 904  
QY 847 CATGTAAACAGCGCTGCAAAAGCTGCTGCGGTAAACAGCGCTGCAAAAGCTGCTGCG 906  
DB 905 CATGTAAACAGCGCTGCAAAAGCTGCTGCGGTAAACAGCGCTGCAAAAGCTGCTGCG 964  
QY 907 GGTAAACAGCGCTGCAAAAGCTGCTGCGGTAAACAGCGCTGCAAAAGCTGCTGCG 966  
DB 965 GGTAAACAGCGCTGCAAAAGCTGCTGCGGTAAACAGCGCTGCAAAAGCTGCTGCG 1024  
QY 967 CCTGAAGAGAGCCCTTATCTGTGCTCAGAGACTCAGAAACCTCTGTGGTCAATGCTCAAT 1026  
DB 1025 CCTGAAGAGAGCCCTTATCTGTGCTCAGAGACTCAGAAACCTCTGTGGTCAATGCTCAAT 1084  
QY 1027 CCCGGAG 1086  
DB 1085 CCCGGAG 1144  
QY 1087 GCTTGGCCAGCTGGAAG 1145  
DB 1145 GCTTGGCCAGCTGGAAG 1204

QY	1146	ACCTGGGGCTTCAAAAGTTGTAATGCGCATGGAATCTTTTGTATGATTTGAATGC	1205
Db	1205	ACCTGGGGCTTCAAAAGTTGTAATGCGCATGGAATCTTTTGTATGATTTGAATGC	1264
QY	1206	AAGATAGTTTATCTAATTCTGCGCAATCAGCTTCTAATCTTGACTTGAATTCGTGCG	1265
Db	1265	AAGATAGTTTATCTAATTCTGCGCAATCAGCTTCTAATCTTGACTTGAATTCGTGCG	1322
QY	1266	AAGAAGATGAGTAATGAGCGAGCCCCCAATATAAATATTCATCG	1309
Db	1325	AAGAAGATGAGTAATGAGCGAGCCCCCAATATAAATATTCATCG	1368
AA160765	standard; cDNA; 1235 BP.		
AA160765;			
22-OCT-2001	(first entry)		
Human	polynucleotide SEQ ID NO 4754.		
Human;	nootropic; immunosuppressant; cyostatic; gene therapy; cancer;		
peripheral	nervous system; neuropathy; central nervous system; CNS;		
Alzheimer's;	Parkinson's disease; Huntington's disease; haemostatic;		
amyotrophic	lateral sclerosis; Shy-Drager Syndrome; chemotactic;		
chemokineic;	thrombolytic; drug screening; arthritis; inflammation;		
leukaemia; ss.			
Homo sapiens.			
WO200153312-A1.			
26-JUL-2001.			
26-DEC-2000;	2000WO-US034263.		
23-DEC-1999;	99US-00471275.		
21-JAN-2000;	2000US-00488725.		
25-APR-2000;	2000US-00523137.		
20-JUN-2000;	2000US-00598042.		
19-JUL-2000;	2000US-00620312.		
03-AUG-2000;	2000US-00653450.		
14-SEP-2000;	2000US-00662191.		
19-OCT-2000;	2000US-00693036.		
29-NOV-2000;	2000US-00727344.		
(HYSE-) HYSEQ INC.			
Tang YT, Liu C, Auandi V, Chen R, Ma Y, Qian XB, Ren F, Wang D, Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA, Zhou P, Goodrich R, Dimaac RT;			
WPI: 2001-442253/47.			
P-PSDB; AAM41609.			
Novel	nucleic acids and polypeptides, useful for treating disorders such		
as	central nervous system injuries.		
Claim 1;	SEQ ID NO 4754; 10078bp; English.		
The	invention relates to human nucleic acids (AA157798-AA161369) and the		
encoded	polypeptides (AAM38642-AA42213) with nootropic,		
immunosuppressant	and cyostatic activity. The polynucleotides are useful		
in	gene therapy. A composition containing a polypeptide or polynucleotide		
of	the invention may be used to treat diseases of the peripheral nervous		
system,	such as peripheral nervous injuries, peripheral neuropathy and		
localised	neuropathies and central nervous system diseases, such as		
Alzheimer's,	Parkinson's disease, Huntington's disease, amyotrophic		
lateral	sclerosis, and Shy-Drager Syndrome. Other uses include the		
utilisation	of the activities such as: Immune system suppression,		
Activin/inhbin	activity, chemotactic/chemokineic activity, haemostatic		

CC	and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC	assays for receptor activity, arthritis and inflammation, leukemias and
CC	C.N.S disorders. Note: The sequence data for this patent did not form
XX	part of the printed specification
XX	
Sequence 1235 BP; 259 A; 359 C; 330 G; 287 T; 0 U; 0 Other;	
Query Match	88.9%; Score 1177; DB 4; Length 1235;
Best Local Similarity	99.7%; Pred. No. 0;
Matches 1221; Conservative	0; Mismatches 0; Indels 4; Gaps 4
QY	1 CTTGAGAGGCTGTGGCTCTGTGCTTTGTTAGGCGGCGCCGAGAGACGGCATGCGGAGCGCCG
Db	3 CTTGAGAGGCTGTGGCTCTGTGCTTTGTTAGGCGGCGCCGAGAGACGGCATGCGGAGCGCCG
QY	61 ACACTGGGAGGAGGAGTCAACGACCCAGCCCGGACCGGCTGTGGGCTGGGAGAGTTGTG
Db	63 ACACTGGGAGGAGGAGTCAACGACCCAGCCCGGACCGGCTGTGGGCTGGGAGAGTTGTG
QY	121 TATTTGGACGAGAGCAGACAGCGCGTGGTCCCTTAACCATTCGATGAATGAAGTATGTTA
Db	123 TATTTGGACGAGAGCAGACAGCGCGTGGTCCCTTAACCATTCGATGAATGAAGTATGTTA
QY	181 CAGTTACGGGTGTCTTGTGCTGTGGAGAACGTGTCCTGTGGGAGGCGCTATGACCCCAAC
Db	183 CAGTTACGGGTGTCTTGTGCTGTGGAGAACGTGTCCTGTGGGAGGCGCTATGACCCCAAC
QY	241 CAGATAGGCCCAAGCTGTGCTGCTATATATGTGGACAGCTCTACCTGATGACGATACCGA
Db	243 CAGATAGGCCCAAGCTGTGCTGCTATATATGTGGACAGCTCTACCTGATGACGATACCGA
QY	301 TCCTCAGACTCAGATTTCTGGCGCTTAGTGTATACACATCAAGATTGACGGCGTGGAGAC
Db	303 TCCTCAGACTCAGATTTCTGGCGCTTAGTGTATACACATCAAGATTGACGGCGTGGAGAC
QY	361 ATGCTTCTCGAGCTGTGCTGCAGATGACTGATGTATGTCCTTGGACAGACCTGTCTCTTT
Db	363 ATGCTTCTCGAGCTGTGCTGCAGATGACTGATGTATGTCCTTGGACAGACCTGTCTCTTT
QY	421 CACCCAGGGGCTGAGCGCTGGCGCAGGCTCAAAATGGGAGATGTGTGTTCTGTTCACCTTC
Db	423 CACCCAGGGGCTGAGCGCTGGCGCAGGCTCAAAATGGGAGATGTGTGTTCTGTTCACCTTC
QY	481 GTTTACTATGCTGTGTCTTCTCCACACAGCTGGGGTCTGGGAGAAATGACACAG
Db	483 GTTTACTATGCTGTGTCTTCTCCACACAGCTGGGGTCTGGGAGAAATGACACAG
QY	541 GATAGAGCTTACCCAGAGGGCGTGGAGACCTGCTGTAGCCCATCTGTGCGCTTAGAC
Db	543 GATAGAGCTTACCCAGAGGGCGTGGAGACCTGCTGTAGCCCATCTGTGCGCTTAGAC
QY	601 TACCACTCTGCGCACAAGA - GGATTCCAATTTGGCAGACCTTCTCAGGTGCCACGTATA
Db	603 TACCACTCTGCGCACAAGAAGGATTCCAATTTGGCAGACCTTCTCAGGTGCCACGTATA
QY	660 CTTGTGCTGGGCTTTTCTCAGCTGAGTATGATGATCTTCAAGCTTTTCTGTCTCTGT
Db	663 CTTGTGCTGGGCTTTTCTCAGCTGAGTATGATGATCTTCAAGCTTTTCTGTCTCTGT
QY	720 CCCTCAGAGCCTAGTATTTCAATTTGACACACCACTCAGTCCGTTAAACCTTGAGAGAC
Db	723 CCCTCAGAGCCTAGTATTTCAATTTGACACACCACTCAGTCCGTTAAACCTTGAGAGAC
QY	780 ACAGCGGATTCACCTGAGCAGACCTTGAACCTTGAAACCTTGAGATCTCAATGATGCT
Db	783 ACAGCGGATTCACCTGAGCAGACCTTGAACCTTGAAACCTTGAGATCTCAATGATGCT
QY	840 ACGCTGCATGTAAACAGCGCTGGAACGCTGCTGCGGTTAAACAGCTGCAAAAGCT
Db	843 ACGCTGCATGTAAACAGCGCTGGAACGCTGCTGCGGTTAAACAGCTGCAAAAGCT
QY	900 GCGTGGCCGTTAAACGCGCTGCAACGCTGCTGCCACAGATTCAAGTGCAGCTCA
Db	902 GCGTGGCCGTTAAACGCGCTGCAACGCTGCTGCCACAGATTCAAGTGCAGCTCA



QY 1113 GGTGGGTTTCCCCC-TTTATAGATGTCACGCACTGGGTGTTACAAAGTTGATG 1171  
DB 4446 GGTGGGTTTCCCCCCTTTATAGATGTCACGCACTGGGTGTTACAAAGTTGATG 4505  
QY 1112 GATATAATCTTTTGTATGATGATTAATGCAAGATGTTATCTTACTGTCGCC 1231  
DB 4506 GATATAATCTTGTGATGATTAATGCAAGATGTTATCTTACTGTCGCC 4565  
QY 1232 AATCAGCTTCTATCCTTGACTAGATTCTGTGAGAGAGATGAGATAGCGGCCCA 1291  
DB 4566 AATCAGCTTCTATCCTTGACTAGATTCTGTGAGAGAGATGAGATAGCGGCCCA 4625  
QY 1292 AATATAAATATTCATGGA 1311  
DB 4626 NATATAAATATTCANGGGA 4645

RESULT 9  
AAA89670  
ID AAA89670 standard; cDNA; 561 BP.  
XX  
AC AAA89670;  
XX  
DT 08-JAN-2001 (first entry)  
XX  
DE Human T cell leukemia/lymphoma 1 nucleotide sequence.  
XX  
KW Exocytosis pathway protein; Exo protein; antiparkinsonian; antidiabetic;  
KW antiallergic; antiaesthetic; neuroprotective; anticonvulsant;  
KW vulnerability; asthma; inflammation; allergy; Chediak-Higashi syndrome; CHS;  
KW Alzheimer's disease; Parkinson's disease; Huntington's disease; diabetes;  
KW digestion disorder; wound healing disorder; gene therapy; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200043419-A2.  
XX  
PD 27-JUL-2000.  
XX  
PF 20-JAN-2000; 2000WO-US001431.  
XX  
PR 20-JAN-1999; 99US-0116534P.  
PR 26-JAN-1999; 99US-0117274P.  
PR 26-JAN-1999; 99US-0117308P.  
PR 26-JAN-1999; 99US-0117309P.  
PR 26-JAN-1999; 99US-0117312P.  
PR 01-FEB-1999; 99US-0118177P.  
PR 01-FEB-1999; 99US-0118178P.  
PR 01-FEB-1999; 99US-0118179P.  
PR 09-FEB-1999; 99US-0119286P.  
PR 11-FEB-1999; 99US-0119759P.  
PR 11-FEB-1999; 99US-0119988P.  
XX  
PA (RIG-) RIGEL PHARM INC.  
XX  
PI Luo Y;  
XX  
DR WPI; 2000-482908/42.  
XX  
PT New nucleic acids encoding Exo proteins which are useful in the  
PT diagnosis, treatment or prevention of exocytosis-mediated disorders such  
PT as asthma, inflammation and allergies.  
XX  
PS Disclosure; Page 251; 305pp; English.  
XX  
XX The present sequence encodes a polypeptide which is associated with the  
CC exocytosis pathway. cDNA molecules encoding proteins involved in  
CC exocytosis have been isolated by yeast one-hybrid and two-hybrid  
CC screening. Novel proteins, termed Exo proteins, have been identified that  
CC interact with known exocytosis-associated proteins such as GS27, alpha  
CC snap, unc18-1, Vamp3, snap-23, and the rab family of proteins. Exo  
CC proteins and their agonists and antagonists are useful in the diagnosis,

CC treatment or prevention of exocytosis-mediated disorders such as asthma,  
CC inflammation, allergies, Chediak-Higashi syndrome (CHS), Alzheimer's  
CC disease, Parkinson's disease, Huntington's disease, diabetes, digestion  
CC disorders and wound healing disorders. The nucleic acids, antagonists or  
CC agonists of Exo proteins are useful in gene therapy. The nucleic acids  
CC are also useful for generating transgenic or knock-out animals which can  
CC be used in the development and screening of therapeutically useful  
CC reagents  
XX  
SQ Sequence 561 BP; 110 A; 160 C; 151 G; 135 T; 0 U; 5 Other;  
Query Match 38.6%; Score 511; DB 3; Length 561;  
Best Local Similarity 98.4%; Pred. No. 4.5e-140;  
Matches 555; Conservative 0; Mismatches 5; Indels 4; Gaps 4;  
QY 104 CTTGGGAGAGTTGCTGTATTTTGGACAGAGACGACGCTGGCTGCTTAACCATCG 163  
DB 1 CTTGGGAGAGTTGCTGTATTTTGGACAGAGACGACGCTGGCTGCTTAACCATCG 60  
QY 164 AGATAAGATAGGTTACAGTTACGGGTGCTTTGGGTGGGAAAGCTGTCCTGGGGA 223  
DB 61 AGATAAGATAGGTTACAGTTACGGGTGCTTTGGGTGGGAAAGCTGTCCTGGGGA 120  
QY 224 GGCCTATGACCCGCCACCCAGATAGGCCCAAGCCTGCTCTATCATGTGACCTTACC 283  
DB 121 GGCCTATGACCCGCCACCCAGATAGGCCCAAGCCTGCTCTATCATGTGACCTTACC 180  
QY 284 CTGATGACGATACCAGTCTCTGAGCTCCAGTTCTTGGCGCTTAAGTACCATCAAGA 343  
DB 181 CTGATGACGATACCAGTCTCTGAGCTCCAGTTCTTGGCGCTTAAGTACCATCAAGA 240  
QY 344 TTGACGGCGTGGAGAGACATGCTCTGAGCTGTGCGCAATGATGATGATGATGATG 403  
DB 241 TTGACGGCGTGGAGAGACATGCTCTGAGCTGTGCGCAATGATGATGATGATGATG 300  
QY 404 CAGACCTGCTCTCTTTCACCCAGGAGCTGAGCCTGAGCCATCAATGGGATGTTG 463  
DB 301 CAGACCTGCTCTCTTTCACCCAGGAGCTGAGCCTGAGCCATCAATGGGATGTTG 360  
QY 464 TGTTCGTTACACCTTCGTTTACTATGCTGTGTCTTTCACACAGCTGGGCTTGGGA 523  
DB 361 TGTTCGTTACACCTTCGTTTACTATGCTGTGTCTTTCACACAGCTGGGCTTGGGA 420  
QY 524 GGAATGACAGACAGAGATGAGCTTACCCAGGAGCTGACAGGACCTGCTGAGCCAC 583  
DB 421 GGAATGACAGACAGAGATGAGCTTACCCAGGAGCTGACAGGACCTGCTGAGCCAC 479  
QY 584 TCTGCTGCTTACGACCTACCTCTGCGAAGAGATTCATTTGGCAGAGCTTCTTC 643  
DB 480 TCTGCTGCTTACGACCTACCTCTGCGAAGAGATTCATTTGGCAGAGCTTCTTC 537  
QY 644 CAGGTGCCAGCATATCTGTCGCC 667  
DB 538 CAGGTGCCAGCATATCTGTGCC 560

RESULT 10  
AAKS4596/c  
ID AAKS4596 standard; cDNA; 285 BP.  
XX  
AC AAKS4596;  
XX  
DT 13-NOV-2001 (first entry)  
XX  
DE Human haematological malignancy-related antigen coding sequence #321.  
XX  
KW Human; cytostatic; vascular; gene therapy; vaccine; lymphoma;  
KW haematological malignancy; antigen; chronic lymphocytic leukemia;  
KW follicular lymphoma; Hodgkin's lymphoma; non-Hodgkin's lymphoma; ss.  
OS Homo sapiens.  
XX  
PN WO200164886-A2.

P	D
X	X
XX	XX
PD	07-SEP--2001.
PF	01-MAR--2001; 200LWO-US007272.
PR	01-MAR--2000; 2000US-0186126P.
PR	17-MAR--2000; 2000US-0190479P.
PR	27-APR--2000; 2000US-0200545P.
PR	28-APR--2000; 2000US-0200303P.
PR	28-APR--2000; 2000US-0200779P.
PR	01-MAY--2000; 2000US-0200999P.
PR	04-MAY--2000; 2000US-0202084P.
PR	22-MAY--2000; 2000US-0206201P.
PR	14-JUL--2000; 2000US-0218950P.
PR	03-AUG--2000; 2000US-0222903P.
PR	04-AUG--2000; 2000US-0223416P.
PR	07-AUG--2000; 2000US-0223378P.
PA	(CORI-) CORIXA CORP.
PI	Gaiser A., Algate PA, Mannion J;
DR	WPI; 2001-514842/56.
PT	Compositions and methods for the detection of hematological malignancies,
PT	e.g. chronic lymphocytic leukemia, lymphoma, follicular lymphoma and
PS	Hodgkin's and T/B cell non-Hodgkin's lymphoma.
PS	Claim 31; Page 417; 1252pp; English.
CC	The present invention relates to compositions and methods for the
CC	detection, diagnosis and therapy of haematological malignancies. The
CC	present sequence is the coding sequence of a human haematological
CC	malignancy related antigen. The methods of the present invention comprise
CC	detecting the presence of haematological malignancy related antigen(s) in
CC	a sample obtained from the patient (an increased level of the
CC	polypeptide, compared to an unaffected individual, is indicative of an
CC	increased risk). Haematological malignancies which can be treated using
CC	the present invention are chronic lymphocytic leukaemia, lymphoma,
CC	follicular lymphoma, Hodgkin's lymphoma, non-Hodgkin's lymphoma and T/B
CC	cell non-Hodgkin's lymphoma
SQ	Sequence 285 BP; 61 A; 63 C; 96 G; 65 T; 0 U; 0 Other;
Query Match	21.5%; Score 285; DB 4; Length 285;
Best Local Similarity	100.0%; Pred. No. 1.7e+73;
Matches 285; Conservative	0; Mismatches 0; Indels 0; Gaps 0
OY	6B2 CTGATGATGGTCTTCAGCCTTTCTGTGCCCTTGTCCTCACACACTAGATTTCATA
DB	285 TTGGTAGTAGGTCTTCAGCCTTTCTGTGCCCTTGTCCTCACACACTAGATTTCATA
OY	742 TGTTGCACAACCACCACTGAGCTCGGTAACTGTGAAGAACAAGCCCATTAACCTGAGCAG
DB	225 TGTTCACAACCACCACTGAGCTCGGTAACTGTGAAGAACAAGCCCATTAACCTGAGCAG
OY	802 ACCCTGAAAACCTCGAACCAAGTGCTTCACATGATGCTACGCGCTGCATGTAAAAACAGCCT
DB	165 ACCTTGAAAACCTCGAACCAAGTGCTTCACATGATGCTACGCGCTGCATGTAAAAACAGCCT
OY	862 GCAAAAGCTGCTGCCTGGTAAACAGCGCTCGCAAACGCTGCGCCCGTAAACAGCGCTGC
DB	105 GCAAAAGCTGCTGCCTGGTAAACAGCGCTCGCAAACGCTGCGCCCGTAAACAGCGCTGC
OY	922 AAACCGCTGCTGCCCAACACAGTTTCAACGTGACAGCTCAAGSAAAG 966
DB	45 AAAAGCTGCTGCCCAACACAGTTTCAACGTGACAGCTCAAGSAAAG 1
RESULT 11	
ID	AASK54743/C standard; cDNA; 285 BP.
XX	XX

AC AAK54743;  
 XX  
 DT 13-NOV-2001 (First entry)  
 DE Human haematological malignancy-related antigen coding sequence #468.  
 XX  
 KW Human; cytosolic; vascular; gene therapy; vaccine; lymphoma;  
 XX haematological malignancy; antigen; chronic lymphocytic leukaemia;  
 XX follicular lymphoma; Hodgkin's lymphoma; non-Hodgkin's lymphoma; ss.  
 OS Homo sapiens.  
 XX  
 PN WO200164886-A2.  
 XX  
 PD 07-SEP-2001.  
 XX  
 PF 01-MAR-2001; 2001WO-US007272.  
 XX  
 PR 01-MAR-2000; 2000US-0186126P.  
 PR 17-MAR-2000; 2000US-0190479P.  
 PR 27-APR-2000; 2000US-0200545P.  
 PR 28-APR-2000; 2000US-0200303P.  
 PR 28-APR-2000; 2000US-0200779P.  
 PR 01-MAY-2000; 2000US-0200999P.  
 PR 04-MAY-2000; 2000US-0202084P.  
 PR 22-MAY-2000; 2000US-0206201P.  
 PR 14-JUL-2000; 2000US-0218950P.  
 PR 03-AUG-2000; 2000US-0222903P.  
 PR 04-AUG-2000; 2000US-0223416P.  
 PR 07-AUG-2000; 2000US-0223378P.  
 XX  
 PA (CORI-) CORIXA CORP.  
 XX  
 PI Gaiger A, Algate PA, Mannion J;  
 XX WPI; 2001-514842/56.  
 XX  
 DR Compositions and methods for the detection of hematological malignancies,  
 PT e.g. chronic lymphocytic leukemia, lymphoma, follicular lymphoma and  
 PT Hodgkin's and T/B cell non-Hodgkin's lymphoma.  
 PT  
 XX  
 PS Claim 31; Page 454; 1252pp; English.  
 XX  
 CC The present invention relates to compositions and methods for the  
 CC detection, diagnosis and therapy of haematological malignancies. The  
 CC present sequence is the coding sequence of a human haematological  
 CC malignancy related antigen. The methods of the present invention comprise  
 CC detecting the presence of haematological malignancy related antigen(s) in  
 CC a sample obtained from the patient (an increased level of the  
 CC polypeptide, compared to an unaffected individual, is indicative of an  
 CC increased risk). Haematological malignancies which can be treated using  
 CC the present invention are chronic lymphocytic leukaemia, lymphoma,  
 CC follicular lymphoma, Hodgkin's lymphoma, non-Hodgkin's lymphoma and T/B  
 CC cell non-Hodgkin's lymphoma  
 XX  
 SQ Sequence 285 BP; 61 A; 63 C; 96 G; 65 T; 0 U; 0 Other;  
 XX  
 Query Match 21.5%; Score 285; DB 4; Length 285;  
 Best Local Similarity 100.0%; Pred. NO. 1.7e-73;  
 Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0  
 DB 682 CTGTGATGATGCTTTCAAGCCTCTTCTCTCCCTTCTGTCCCTCAGACGACTGATTTTCA 741  
 DB 285 CTGTGATGATGCTTTCAAGCCTCTTCTCTCCCTTCTGTCCCTCAGACGACTGATTTTCA 226  
 QY 742 TGTTCGACACCCACTGAGCTCCGTGAACCTTGTGAGAACACAGCCGATTCACCTGAGCAG 801  
 DB 225 TGTTCGACACCCACTGAGCTCCGTGAACCTTGTGAGAACACAGCCGATTCACCTGAGCAG 166  
 QY 802 ACCCTGTGAACCCCTGAGACCACTGTGCTTCACATGGCGTCAACGCTGCAATGTAACAGCGCT 861  
 DB 165 ACCCTGTGAACCCCTGAGACCACTGTGCTTCACATGGCGTCAACGCTGCAATGTAACAGCGCT 106

QY 862 GCAAAAGCTGCTGCGGTAAACACGCTGCAAAAGCTGCTGCGGTAAACACGCTGCG 921  
 DB 105 GCAAAAGCTGCTGCGGTAAACACGCTGCAAAAGCTGCTGCGGTAAACACGCTGCG 46  
 QY 922 AAACGCTGCTGCGGTAAACACGCTGCAAAAGCTGCTGCGGTAAACACGCTGCG 966  
 DB 45 AAACGCTGCTGCGGTAAACACGCTGCAAAAGCTGCTGCGGTAAACACGCTGCG 1

## RESULT 12

AAK54793/c  
 ID AAK54793 standard; cDNA, 285 BP.

AAK54793;  
 AC AAK54793;  
 XX AAK54793;  
 XX AAK54793;  
 DT 13-NOV-2001 (first entry)

DE Human haematological malignancy-related antigen coding sequence #518.

KW Human; cytostatic; vascular; gene therapy; vaccine; lymphoma;  
 KW haematological malignancy; antigen; chronic lymphocytic leukaemia;  
 KW follicular lymphoma; Hodgkin's lymphoma; non-Hodgkin's lymphoma; ss.

OS Homo sapiens.

PN WO200164886-A2.

PD 07-SEP-2001.

PF 01-MAR-2001; 2001WO-US007272.

PR 01-MAR-2000; 2000US-0186126P.  
 PR 17-MAR-2000; 2000US-0190479P.  
 PR 27-APR-2000; 2000US-0200545P.  
 PR 28-APR-2000; 2000US-0200303P.  
 PR 28-APR-2000; 2000US-0200779P.  
 PR 01-MAY-2000; 2000US-0200999P.  
 PR 04-MAY-2000; 2000US-0202084P.  
 PR 22-MAY-2000; 2000US-0206201P.  
 PR 14-JUL-2000; 2000US-0218950P.  
 PR 03-AUG-2000; 2000US-0222903P.  
 PR 04-AUG-2000; 2000US-0223416P.  
 PR 07-AUG-2000; 2000US-0223378P.

PA (CORI-) CORIXA CORP.

PI Gaiger A, Algate PA, Mannion J;

DR WPI; 2001-514842/56.

XX Compositions and methods for the detection of hematological malignancies,  
 PT e.g. chronic lymphocytic leukemia, lymphoma, follicular lymphoma and  
 PT Hodgkin's and T/B cell non-Hodgkin's lymphoma.

PS Claim 31; Page 467; 1252pp; English.

XX The present invention relates to compositions and methods for the  
 CC detection, diagnosis and therapy of haematological malignancies. The  
 CC present sequence is the coding sequence of a human haematological  
 CC malignancy related antigen. The methods of the present invention comprise  
 CC detecting the presence of haematological malignancy related antigen(s) in  
 CC a sample obtained from a patient (an increased level of the  
 CC polypeptide, compared to an unaffected individual, is indicative of an  
 CC increased risk). Haematological malignancies which can be treated using  
 CC the present invention are chronic lymphocytic leukaemia, lymphoma,  
 CC follicular lymphoma, Hodgkin's lymphoma, non-Hodgkin's lymphoma and T/B  
 CC cell non-Hodgkin's lymphoma

PS Sequence 285 BP; 62 A; 63 C; 95 G; 65 T; 0 U; 0 Other;

XX Query Match 21.4%; Score 283.4; DB 4; Length 285;  
 CC Best Local Similarity 99.6%; Pred. No. 5e-73;  
 CC Matches 284; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 682 CTGATATATGCTCTTGACGCTCTTTCTGTCCCTTTCTGTCCCTGACACACTAGTATTTC 741  
 DB 285 CTGATATATGCTCTTGACGCTCTTTCTGTCCCTTTCTGTCCCTGACACACTAGTATTTC 226  
 QY 742 TGTTCACACCCACTAGCTCCGTGAACCTGTGAACACAGCCGATTCACCTGAGCAG 801  
 DB 225 TGTTCACACCCACTAGCTCCGTGAACCTGTGAACACAGCCGATTCACCTGAGCAG 166  
 QY 802 ACCTTGAACCCCTGACACAGGTGCTCACATGTGTCTACGCTGACATGTTAAACAGCCT 861  
 DB 165 ACCTTGAACCCCTGACACAGGTGCTCACATGTGTCTACGCTGACATGTTAAACAGCCT 106  
 QY 862 GCAAAAGCTGCTGCGGTAAACACGCTGCAAAAGCTGCTGCGGTAAACACGCTGCG 921  
 DB 105 GCAAAAGCTGCTGCGGTAAACACGCTGCAAAAGCTGCTGCGGTAAACACGCTGCG 46  
 QY 922 AAACGCTGCTGCGGTAAACACGCTGCAAAAGCTGCTGCGGTAAACACGCTGCG 966  
 DB 45 AAACGCTGCTGCGGTAAACACGCTGCAAAAGCTGCTGCGGTAAACACGCTGCG 1

## RESULT 13

AAK54693/c  
 ID AAK54693 standard; cDNA, 285 BP.

AAK54693;  
 AC AAK54693;  
 XX AAK54693;  
 XX AAK54693;  
 DT 13-NOV-2001 (first entry)

DE Human haematological malignancy-related antigen coding sequence #418.

KW Human; cytostatic; vascular; gene therapy; vaccine; lymphoma;  
 KW haematological malignancy; antigen; chronic lymphocytic leukaemia;  
 KW follicular lymphoma; Hodgkin's lymphoma; non-Hodgkin's lymphoma; ss.

OS Homo sapiens.

PN WO200164886-A2.

PD 07-SEP-2001.

PF 01-MAR-2001; 2001WO-US007272.

PR 01-MAR-2000; 2000US-0186126P.  
 PR 17-MAR-2000; 2000US-0190479P.  
 PR 27-APR-2000; 2000US-0200545P.  
 PR 28-APR-2000; 2000US-0200303P.  
 PR 28-APR-2000; 2000US-0200779P.  
 PR 01-MAY-2000; 2000US-0200999P.  
 PR 04-MAY-2000; 2000US-0202084P.  
 PR 22-MAY-2000; 2000US-0206201P.  
 PR 14-JUL-2000; 2000US-0218950P.  
 PR 03-AUG-2000; 2000US-0222903P.  
 PR 04-AUG-2000; 2000US-0223416P.  
 PR 07-AUG-2000; 2000US-0223378P.

PA (CORI-) CORIXA CORP.

PI Gaiger A, Algate PA, Mannion J;

DR WPI; 2001-514842/56.

XX Compositions and methods for the detection of hematological malignancies,  
 PT e.g. chronic lymphocytic leukemia, lymphoma, follicular lymphoma and  
 PT Hodgkin's and T/B cell non-Hodgkin's lymphoma.

PS Claim 31; Page 442; 1252pp; English.

XX The present invention relates to compositions and methods for the  
 CC detection, diagnosis and therapy of haematological malignancies. The  
 CC present sequence is the coding sequence of a human haematological  
 CC malignancy related antigen. The methods of the present invention comprise







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OM nucleic - nucleic search, using sw model

Run on: June 17, 2004, 10:59:20 ; Search time 5328 Seconds  
(without alignment)  
10770.679 Million cell updates/sec

Title: US-09-441-242A-1  
Perfect score: 1324  
Sequence: 1 ctctgagagagcctcgcctctt.....catgaaaaaaaaaaaaaa 1324

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

- 1: GenEmbl:\*
- 2: gb\_ba:\*
- 3: gb\_hcg:\*
- 4: gb\_in:\*
- 5: gb\_ov:\*
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- 11: gb\_scs:\*
- 12: gb\_sy:\*
- 13: gb\_un:\*
- 14: gb\_vl:\*
- 15: em\_ba:\*
- 16: em\_fun:\*
- 17: em\_hum:\*
- 18: em\_in:\*
- 19: em\_mu:\*
- 20: em\_om:\*
- 21: em\_ov:\*
- 22: em\_ov:\*
- 23: em\_pat:\*
- 24: em\_ph:\*
- 25: em\_pl:\*
- 26: em\_ro:\*
- 27: em\_scs:\*
- 28: em\_un:\*
- 29: em\_vl:\*
- 30: em\_hcg\_hum:\*
- 31: em\_hcg\_inv:\*
- 32: em\_hcg\_other:\*
- 33: em\_hcg\_mus:\*
- 34: em\_hcg\_pln:\*
- 35: em\_hcg\_rtd:\*
- 36: em\_hcg\_mam:\*
- 37: em\_hcg\_vrt:\*
- 38: em\_gv:\*
- 39: em\_htgo\_hum:\*
- 40: em\_htgo\_mus:\*
- 41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1324	100.0	1324	6 AR086519	AR086519 Sequence
2	1324	100.0	1324	6 AX237689	AX237689 Sequence
3	1324	100.0	1324	9 HSTC1	X82240 H. sapiens m
4	1280	96.7	1368	6 AR339380	AR339380 Sequence
5	1187	89.7	1231	9 BC003574	BC003574 Homo sapi
6	1187	89.7	1231	9 BC005831	BC005831 Homo sapi
7	925	69.9	925	11 G26659	G26659 human STR S
8	902.4	68.2	166308	9 CNS01DX2	AL139020 Human chr
9	894	67.5	938	9 BC009502	BC009502 Homo sapi
10	894	67.5	938	9 BC009891	BC009891 Homo sapi
11	819.8	61.9	4922	6 AR086521	AR086521 Sequence
12	285	21.5	285	6 AX237345	AX237345 Sequence
13	285	21.5	285	6 AX237492	AX237492 Sequence
14	283.4	21.4	285	6 AX237442	AX237442 Sequence
15	283.4	21.4	285	6 AX237542	AX237542 Sequence
16	283	21.4	318	6 AX237315	AX237315 Sequence
17	283	21.4	318	6 AX237473	AX237473 Sequence
18	240	18.1	240	6 AX237350	AX237350 Sequence
19	235	17.7	240	6 AX237343	AX237343 Sequence
20	225	17.0	228	6 AX237353	AX237353 Sequence
21	189.8	14.3	221	6 AX237334	AX237334 Sequence
22	167.8	12.7	3716	6 AX598716	AX598716 Sequence
23	159.4	12.0	1392	10 BC052336	BC052336 Mus muscu
24	157.8	11.9	1338	10 MMRNATC1	Y15376 Mus musculu
25	157.8	11.9	1338	10 AF031956	AF031956 Mus muscu
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27	107.6	8.1	3716	6 AX346684	AX346684 Sequence
28	102	7.7	3716	6 AX598866	AX598866 Sequence
29	102	7.7	6716	6 AX346685	AX346685 Sequence
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33	85	6.4	270378	2 AC096495	AC096495 Rattus no
34	81.2	6.1	3716	6 AX599012	AX599012 Sequence
35	80.2	6.1	248983	10 AC124777	AC124777 Mus muscu
36	65	4.9	560	6 AR086520	AR086520 Sequence
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38	63.4	4.8	3240	9 AB035342	AB035342 Homo sapi
39	62.8	4.7	1152	9 AF110466	AF110466 Homo sapi
40	62.8	4.7	1177	9 AF137027	AF137027 Homo sapi
41	62.8	4.7	1144	9 AB035343	AB035343 Homo sapi
42	62.8	4.7	3532	9 AB035340	AB035340 Homo sapi
43	62.8	4.7	3599	9 AB035341	AB035341 Homo sapi
44	61.2	4.6	1169	9 BC051000	BC051000 Homo sapi
45	61.2	4.6	1722	9 AB018563	AB018563 Homo sapi

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES
AR086519	AR086519	Sequence 1 from patent US 5985598.	AR086519	AR086519.1	GI:10013285	Unknown.	Unknown.	1 (bases 1 to 1324)	Russo,G. and Croce,C.M.	TCP-1 gene and protein and related methods and compositions	US 5985598-A 1 16-NOV-1999;	Location/Qualifiers

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1324; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 CTTGAGAGGCTGCTGCTCTTGTCTTTAGGCGGCCCCGAGAGCCATGCGCGAGTGGCCG 60
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QY 241 CAGATAGGCCCAAGCCTGCTGCTATCATGTGAGCAGCTCTACCCATGAGACGATACGA 300
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QY 361 ATGCTTCTGAGCTGCTGCTGCTGAGATGATGATGCTTGGAGAGACCTGCTCCCTT 420
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RESULT 2
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LOCUS AX237689
DEFINITION Sequence 665 from Patent WO0164886.
ACCESSION AX237689
VERSION AX237689.1 GI:15797243
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
1 Gaiger, A., Algate, P. A. and Mannion, J.
AUTHORS Compositions and methods for the detection, diagnosis and therapy
TITL of hematological malignancies
JOURNAL Patent: WO 0164886-A 665 07-SEP-2001;
CORIXA CORPORATION (US)
FEATURES
Location/Qualifiers
1. .1324
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1324; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGAGAGGCTGCTGCTCTTGTCTTTAGGCGGCCCCGAGAGCCATGCGCGAGTGGCCG 60
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DB 121 TATTTGAGACGAGACGACGAGCGCTGCGCTTAAACATCGAGATTAAGATAGTTA 180
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Db      1321  AAAA 1324

RESULT 3
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DEFINITION H.STCL1 1324 bp mRNA linear PRI 13-MAY-1995
ACCESSION X82240
VERSION X82240.1 GI:624960
KEYWORDS TCLI gene.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Virgilio, L., Narducci, M.G., Isobe, M., Billips, L.G., Cooper, M.D.,
          Croce, C.M. and Russo, G.
TITLE Identification of the TCLI gene involved in T-cell malignancies
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 91 (26), 12530-12534 (1994)
MEDLINE 95107991
PUBMED 7809072
REFERENCE 2 (bases 1 to 1324)
AUTHORS Russo, G.
TITLE Direct Submission
JOURNAL Submitted (19-OCT-1994) G. Russo, Raggio-Italgene SpA, Via delle
          Antille 29, 00040 Pomezia, Rome, ITALY
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QY      121 TATTTGACGAGACGACGACGCTTGCTCCCTTAACATCGAGATAAAGATAGTTA 180
DB      121 TATTTGACGAGACGACGACGCTTGCTCCCTTAACATCGAGATAAAGATAGTTA 180
QY      181 CAGTTACGGGTGCTCTTGCGCTCGGAGAGACGTGCTCTGCGGAGGCGCTATGACCCACC 240
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DEFINITION Sequence 871 from patent US 6569662.  
ACCESSION AR339380  
VERSION AR339380.1 GI:3376237  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1368)  
AUTHORS Tang, Y.T., Zhou, P. and Dymanac, R.T.  
TITLE Nucleic acids and polypeptides  
JOURNAL Patent: US 6569662-A 871 27-MAY-2003;  
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Qy 68 GGGAGCAGTCAACGACACCGGACCGGCTGAGGAGTGTGATTTGG 127  
Db 125 GGGAGCAGTCAACGACACCGGACCGGCTGAGGAGTGTGATTTGG 184  
Qy 128 ACAGAGAGCAGCAGCTGCTGCTGCTTAACTGAGATTAAGATGATGATG 187  
Db 185 ACAGAGAGCAGCAGCTGCTGCTGCTTAACTGAGATTAAGATGATGATG 244  
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Db 245 GGGTCTTGTGCGGAGAGAGTGTGCTGAGGAGCTTGAACCCCAACCGATG 304  
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Db 305 GCCCAAGCTGTGCTTATCATGTGAGCTTACCTGATGAGATCCGATCCTGAG 364  
Qy 308 ACTCAAGTTTCTGGGCTTATGATGACCATTAAGATTTGAGGCTGAGACATGCTTC 367  
Db 365 ACTCAAGTTTCTGGGCTTATGATGACCATTAAGATTTGAGGCTGAGACATGCTTC 424  
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Db 425 TCGAGCTGTGCGCAGATGATGATGATGATGATGATGATGATGATGATGATG 484  
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Db 605 TCTACCAAGGAGCTGAGAGCTGAGCTGATGAGCTGCTGCTTGAAGTACCACT 664  
Qy 608 CTTGCAAGAGAGATTCATTTGGAGAGTCTTCA-GGTGCAGCTATACCTGTGC 666  
Db 665 CTTGCAAGAGAGATTCATTTGGAGAGTCTTCAAGGAGTGCAGCTATACCTGTGC 724

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QY	727	AGCACTAGTATTTCAATGTTGCAACACCACTACGCTCCGTGAACCTTGAGAAACAGACCG	786
Db	785	AGCACTAGTATTTCAATGTTGCAACACCACTACGCTCCGTGAACCTTGAGAAACAGACCG	844
QY	787	ATTCACTGAGACAGAACCTCTGAAACCTTGACACAGTGGTCTCAATGCTGTAAGCTGG	846
QY	845	ATTCACTGAGACAGAACCTCTGAAACCTTGACACAGTGGTCTCAATGCTGTAAGCTGG	904
QY	847	CATGTAACAAGCCCTGCAAAACGCTGCTGCGGTGAACACGCGCTGCAACGCTGCTGCC	906
Db	905	CATGTAACAAGCCCTGCAAAACGCTGCTGCGGTGAACACGCGCTGCAACGCTGCTGCC	964
QY	907	CGTAAACACGCGCTGCAAAACGCTGCTGCGCGCACACAGTTACGTGACGCTCAAGGAAG	966
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QY	967	CCTGAAGAAGAGCCCTTATCTGTGCTCAGAGACTCAGAACGCTGTGGGTCAAGTGTCAAT	1022
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QY	1027	CCCGGAGACGACAGCAGAGAGCCAGCGCGGAGCCCTGTGAGATGACCCCTCAGAACCTTTG	1086
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QY	1146	ACCTGGGAGTTTCAACAAGTTGATATGAGGATGAATCTTTTGTATGATGATTAATGCG	1202
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QY	1206	AAGATAGTTTATCTAACTTCTGCGGCAATCAGCTTCTAATCCTTGACTTAAGATTCGTGG	1265
Db	1265	AAGATAGTTTATCTAACTTCTGCGGCAATCAGCTTCTAATCCTTGACTTAAGATTCGTGG	1322
QY	1266	AGAGAGTGAAGATATGCGACCCCAATATATATATATTCATGG	1309
Db	1325	AGAGAGTGAAGATATGCGACCCCAATATATATATATTCATGG	1368
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DEFINITION			Homo sapiens T-cell leukemia/lymphoma 1a, mRNA (CDNA clone MGC:226607)
ACCESSION			IMAGE:3544215), complete cds.
VERSION			BC003574
KEYWORDS			BC003574.1 GI:13097749
SOURCE			MGC.
ORGANISM			Homo sapiens (human)
REFERENCE			Homo sapiens
AUTHORS			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1231)
			Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stepleson, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Uebelin, F.B., Tomshinsky, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Wooley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Holys, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Patney, J., Helton, E., Kettelman, M., Madan, A.C., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

TITLE	JOURNAL	MEDLINE	PUBMED	REFERENCE	AUTHORS	TITLE	JOURNAL	REMARK	COMMENT
22388257	22388257	22388257	12477932	2 (bases 1 to 1231)	Strausberg,R. Direct Submission	Submitted (20-FEB-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2550, USA	NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a> Contact: MGC help desk Email: <a href="mailto:cgabs-remail.nih.gov">cgabs-remail.nih.gov</a> Tissue Procurement: Louis M. Staudt, M.D., Ph.D. DNA Library Preparation: Rubin Laboratory DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada <a href="mailto:info@cgsc.bc.ca">info@cgsc.bc.ca</a>	Steven Jones, Jennifer Agano, Ian Boedeltje, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letlicia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Nees, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smalls, Michael Smith, Lorraine Spence, Jeff Sroct, Michael Thorne, Miranda Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Zaira.	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <a href="http://image.lnl.gov">http://image.lnl.gov</a> Series: IRAL Plate: 8 Row: d Column: 6 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4504510. Location/Qualifiers
FEATURES	SOURCE	gene	CDS	misc_feature	misc_feature	misc_feature	misc_feature		
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1. 1231	/gene="TCL1A"	/note="synonym: TCL1"	/db_xref="locusid:8115"	/db_xref="mm:166960"	43. 387	/codon_start=1	/product="T-cell lymphoma-1"	/protein_id="AA03574.1"	/db_xref="gi:13097750"
43. 387	/db_xref="locusid:8115"	/translation="MADCPVLGEAVTDHPDRLMAKEFYVLDKQKALPLPTIEIDR LQIRVLRLREDVVLGRPMPTPTQIGPLPLPMQLYPDGRYSSDFWRLVYIKIDG VEDMLRLPPD"	58. 171	/note="TCL1 MTCP1; Region: TCL1/MTCP1 family. Two related oncogenes, TCL1 and MTCP-1, are overexpressed in T cell prolymphocytic leukemias as a result of chromosomal rearrangements that involve the translocation of one T cell receptor gene to either chromosome 14q32 or Xq28"	232. 384	/note="TCL1 MTCP1; Region: TCL1/MTCP1 family. Two related oncogenes, TCL1 and MTCP-1, are overexpressed in T cell			



http://www.systembiology.org  
contact: amadan@systembiology.org  
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIN ac: <http://image.llnl.gov>  
Series: IRAL Plate: 3 Row: 6 Column: 9  
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 11415027.

## FEATURES

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58..171  
/note="TCL1, MTCPI, Region: TCL1/MTCPI family. Two related  
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## CDS

## misc\_feature

## misc\_feature

Query Match 89.7%; Score 1187; DB 9; Length 1231;  
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Matches 1213; Conservative 0; Mismatches 0; Indels 6; Gaps 2;

## ORIGIN

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304 TCAGCTCCAGTTTCTGGGCGCTTAGTGTACCAATCAAGATTGAGGGGTGGAGACATG 363  
301 TCAGCTCCAGTTTCTGGGCGCTTAGTGTACCAATCAAGATTGAGGGGTGGAGACATG 360  
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361 CTTCGAGCTGCTGCCAGATGATGATGTGCTTGGGAGACACTGTCTCTTTCAC 415  
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596 CACTCTGCGCAAGAGATTCATTTGGGAGAGCTTCTTCCAGGTGCCAGCTATACCTG 655  
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1024 CATCCCGGAGAGGAGAGAGGCGGCGGAGGCGGAGGCTGTGATGAGCCCTCAGAACCC 1083  
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RESULT 7  
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DEFINITION human STS X82240, sequence tagged site.  
ACCESSION G26659.1 GI:134891  
VERSION  
KEYWORDS STS; STS sequence; primer; sequence tagged site.



SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS 1 (bases 1 to 925)  
TITLE Whitehead Institute/MIT Center for Genome Research; Physically  
JOURNAL Mapped Sts  
COMMENT Unpublished (1995)  
Contact: Thomas Hudson  
Whitehead Institute/MIT Center for Genome Research  
9 Cambridge Center, Cambridge MA 02142 USA  
Tel: 617 252 1900  
Fax: 617 252 1902  
Email: thudson@genome.wi.mit.edu  
Primer A: TCCTGGAGCAGCCTGTCTC  
Primer B: GTGGTAGTCTAAGCGCAGC  
STS size: 209  
PCR Profile:  
Denaturation:  
Annealing: 56 degrees C  
Polymerization:  
PCR Cycles: 35  
Thermal Cycler:  
Protocol:  
Template: 10 ng  
Primer: each 5 pM  
dNTPs: each 4 mM  
Taq Polymerase: 0.025 units/ul  
Total Vol: 20 ul  
Buffer:  
MgCl2: 1.5 mM  
KCl: 50 mM  
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Derived from dbEST (Genbank accession X82240).  
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complement(200..219)  
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Best Local Similarity 100.0%; Pred. No. 1e-246;  
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Db 61 TACAAATGGGATGTTGTTCTTCTGTTCACCTTGTCTTACTATGCTGTCTTCTCCACC 120  
QY 508 ACCGTGGGCTCTGGAGGAATGACAGACAGAGATGAGCTTACCCAGGCTGGCAGGA 567  
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QY 628 TTGGCAGAGCTTCTTCCAGGTGCCCACTATACCTGTGCTTGTCTTCTCAGCTGGAT 687  
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LOCUS Human chromosome 14 DNA sequence BAC R-164H13 of library RPCT-11  
DEFINITION from chromosome 14 of Homo sapiens (Human), complete sequence.  
ACCESSION AL139020  
VERSION AL139020.5 GI:13539193  
KEYWORDS HTG.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS 1 (bases 1 to 166308)  
TITLE Helwig, R., Petit, J.L., Vico, V., Dasilva, C., Robert, C., Mincker, P.,  
Brotier, P., Catolico, L., Barde, V., Pelletier, E., Arizguenave, F.,  
Levy, M., Eckenberg, R., Brula, T., deBerardins, V., Craud, C.,  
Gyapay, G., Saurin, W. and Weissbach, J.  
JOURNAL Sequencing of the human chromosome 14  
REFERENCE 2 (bases 1 to 166308)  
AUTHORS Unpublished  
TITLE Direct Submission  
JOURNAL Genoscope.  
BP 191 91006 EVRY cedex - FRANCE (E-mail: sequef@genoscope.cns.fr)



COMMENT

- Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
On Apr 3, 2001 this sequence version replaced gi:1274871.  
----- Genome Center  
Center: Genoscope / Centre National de Sequencage  
Center code: GS  
Web site: <http://www.genoscope.cns.fr/>  
Contact: [SegeRef@genoscope.cns.fr](mailto:SegeRef@genoscope.cns.fr)  
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The following BAC sequence is oriented from the T7 to the SP6 end.  
Upstream BAC (overlapping the T7 end) : R-1070N10  
Downstream BAC (overlapping the SP6 end) : R-185P18 (AC=AL13167)  
----- Summary Statistics  
Assembly program: Phrap; version 2.0  
Quality coverage: 6.03x in Q20 bases; sum-of-contigs

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Overall quality chart :  
Range : bases

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0 :
1 - 9 : 4
10 - 19 : 53
20 - 29 : 203
30 - 39 : 622
40 - 49 : 3717
50 - 59 : 8215
60 - 69 : 11927
70 - 79 : 27324
80 - 89 : 52859
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Percentage of bases with a quality value >= 40 : 99 %.

FEATURES

source

Location/Qualifiers

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Matches 914; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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RESULT 9  
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LOCUS BC009502  
DEFINITION Homo sapiens T-cell leukemia/lymphoma 1A, mRNA (cDNA clone  
IMAGE:4054525), partial cds.  
ACCESSION BC009502



REFERENCE 1 (bases 1 to 938)  
AUTHORS Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stjepanovich M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheer T.E., Brownstein M.J., Uedon T.B., Tohliyoki S., Carninci P., Prange C., Rana S.S., Igoe N.A., Peters G.J., Abramson R.D., Mullaney S.J., Bosak S.A., McEwan P.J., McEwan R.J., Malek J.A., Gunaratne P.H., Richards S., Wollan K.C., Hale S., Garcia A.M., Gay L.J., Hallyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A., Whiting M., Madan A., Young A.C., Shcherchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S., Krzywinski M.I., Skalek U., Smalits D.E., Schermer A., Schein J.E., Jones S.J. and Marra M.A.  
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL MEDLINE 22388257  
PUBMED 12477932  
REFERENCE 2 (bases 1 to 938)  
AUTHORS Straube R.  
JOURNAL Direct Submission  
Submitted (02-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
On Aug 19, 2003 this sequence version replaced gi:14602756.  
REMARK COMMENT  
Contact: MGC help desk  
Email: [gcgdb-remail.nih.gov](mailto:gcgdb-remail.nih.gov)  
Tissue Procurement: Louis Staudt  
DNA Library Preparation: Rubin Laboratory  
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
http://www.systemsbio.org  
Contact: [amadan@systemsbio.org](mailto:amadan@systemsbio.org)  
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha Madan, Stephanie Rodriguez, Amy Sanchez and Michelle Whiting  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAL Plate: 25 Row: 0 Column: 18.  
Location/Qualifiers  
1..938  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/clone="IMAGE:4054422"  
/issue\_type="Primary B-Cells from Tonsils"  
/clone\_id="NIH MGC\_48"  
/lab\_host="DH10B-R"  
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ORIGIN  
Query Match 67.5%; Score 894; DB 9; Length 938;  
Best Local Similarity 99.4%; Pred. No. 4,66-238;  
Matches 920; Conservative 0; Mismatches 0; Indels 6; Gaps 2;

QY 297 CCGATCTCAAGCTTCTGCGCTTGTAGTACATCAAGATTGACGGGTGGA 356  
DB 1 CCGATCTCAAGCTTCTGCGCTTGTAGTACATCAAGATTGACGGGTGGA 60  
QY 357 GGACATGCTTCTGCGCTTGTAGTACATCAAGATTGACGGGTGGA 416  
DB 61 GGACATGCTTCTGCGCTTGTAGTACATCAAGATTGACGGGTGGA 115  
QY 417 CTTTACCCCAAGGCGCTGAGCTGCGCAAGCTTCAATGGGATGTTGTTCTGTTAC 476

DB 116 CTTTACCCCAAGGCGCTGAGCTGCGCAAGCTTCAATGGGATGTTGTTCTGTTAC 175  
QY 477 CTTGTTTACATACCTGCTGCTTCTCCACACCGCTGGGGTCTGGAGAAATGACACAC 536  
DB 176 CTTGTTTACATACCTGCTGCTTCTCCACACCGCTGGGGTCTGGAGAAATGACACAC 235  
QY 537 AGAGATGAGCTTACACCGAGGCGCTGAGACCTGCTGAGCCACTCTGCGCTTGA 596  
DB 236 AGAGATGAGCTTACACCGAGGCGCTGAGACCTGCTGAGCCACTCTGCGCTTGA 295  
QY 597 GCATCAACCTCTGCGCAAGAGATTCTGAGAGAGCTTCTGAGGTGCGCAAGCT 656  
DB 296 GCATCAACCTCTGCGCAAGAGATTCTGAGAGAGCTTCTGAGGTGCGCAAGCT 355  
QY 657 ATACTGTGCTGCGCTTCTGAGCTGAGATGATGATGATGATGATGATGATGATGAT 716  
DB 356 ATACTGTGCTGCGCTTCTGAGCTGAGATGATGATGATGATGATGATGATGATGAT 415  
QY 717 TGTCCCTCAGACACTGATATTTGATGATGATGATGATGATGATGATGATGATGAT 776  
DB 416 TGTCCCTCAGACACTGATATTTGATGATGATGATGATGATGATGATGATGATGAT 475  
QY 777 AACACAGCCGATTCACCTGACAGACCTCTGAAACCTGAGACAGTGTCTCATGAT 836  
DB 476 AACACAGCCGATTCACCTGACAGACCTCTGAAACCTGAGACAGTGTCTCATGAT 535  
QY 837 GCTACGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 896  
DB 536 GCTACGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 595  
QY 897 GCTGCTGCGCCGCTTAAACAGCGCTGCAAAAGCTGCTGCGCCGACAGAGTTTCAAGT 956  
DB 596 GCTGCTGCGCCGCTTAAACAGCGCTGCAAAAGCTGCTGCGCCGACAGAGTTTCAAGT 655  
QY 957 CAAGAAAGGCTGTAAGAGAGCCCTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1016  
DB 656 CAAGAAAGGCTGTAAGAGAGCCCTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 715  
QY 1017 TGTGTCACATCCCGGAGACGACGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCT 1076  
DB 716 TGTGTCACATCCCGGAGACGACGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCT 775  
QY 1077 AGAACCTGCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 1135  
DB 776 AGAACCTGCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 835  
QY 1136 ATGTCACGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1195  
DB 836 ATGTCACGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 895  
QY 1196 GATTAAATGCAAGTATGTTATCTTAA 1221  
DB 896 GATTAAATGCAAGTATGTTATCTTAA 921

RESULT 11  
AK086521  
LOCUS AR086521 4922 bp DNA linear PAT 07-SEP-2000  
DEFINITION Sequence 5 from patent US 5985598.  
ACCESSION AR086521  
VERSION AR086521.1 GI:10013287  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 4922)  
AUTHORS Russo G. and Croce C.M.  
TITLE TGL-1 gene and protein and related methods and compositions  
JOURNAL Patent: US 5985598-A 5 16-NOV-1999;  
FEATURES  
1..4922  
Location/Qualifiers  
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ORIGIN

Query Match 61.9%; Score 819.8; DB 6; Length 4922;  
Best Local Similarity 92.8%; Pred. No. 3e-217;  
Matches 854; Conservative 28; Mismatches 34; Indels 4; Gaps 4;

QY 396 GGTCTTGGAGACCTGTCTCTTCAACCCGAGGAGCTGAGCCCTGAGCCAGCTTCAATGG 455  
DB 3726 GGTCTTGGAGACCTGTCTCTTCAACCCGAGGAGCTGAGCCCTGAGCCAGCTTCAATGG 3785

QY 456 GGAATGTTGTCTTCTTCAACCTTCTTCAATGAGCTGTCTTCTTCTTCAACAGCTGGG 515  
DB 3786 GGAATGTTGTCTTCTTCAACCTTCTTCAATGAGCTGTCTTCTTCTTCAACAGCTGGG 3845

QY 516 GTCTGGAGAGATGAGACAGACAGAGATGAGCTTACCCAGGAGCTGAGAGAGCTG-CCT 574  
DB 3846 GTCTGGAGAGATGAGACAGACAGAGATGAGCTTACCCAGGAGCTGAGAGAGCTG-CCT 3905

QY 575 GTAGCCCACTCTGTCTGCTTGAACA-CTACCACTCTGAGCAAGAGAGATTCATTTGGCA 633  
DB 3906 GTAGCCCACTCTGTCTGCTTGAACA-CTACCACTCTGAGCAAGAGAGATTCATTTGGCA 3965

QY 634 GAGCTTCTTCCAGAGTCCAGACTATACCTGTGCTGCTGCTTCTTCTTCAAGCTGAGATGCT 693  
DB 3966 GAGCTTCTTCCAGAGTCCAGACTATACCTGTGCTGCTGCTTCTTCTTCAAGCTGAGATGCT 4025

QY 694 CTTGAGCCTCTTCTGCTGCTTCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 753  
DB 4026 CTTGAGCCTCTTCTGCTGCTTCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4085

QY 754 ACTGAGCTCGGTGAATCTTGTGAGAACACAGCCGATTCACCTGAGCAGAGACTCTGAAACC 813  
DB 4086 ACTGAGCTCGGTGAATCTTGTGAGAACACAGCCGATTCACCTGAGCAGAGACTCTGAAACC 4145

QY 814 CTGAGCAGAGTGTCTCAATGAGTGTCTACGCTGATGTAACAGAGCTGCAAGAGCTGCC 873  
DB 4146 CTGAGCAGAGTGTCTCAATGAGTGTCTACGCTGATGTAACAGAGCTGCAAGAGCTGCC 4205

QY 874 TGCCGCTTAAACAGCCCTGCAAAAC-GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 932  
DB 4206 TGCCGCTTAAACAGCCCTGCAAAAC-GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4265

QY 933 GCCCAACAGGTTACGCTGACGCTCAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 992  
DB 4266 GCCCAACAGGTTACGCTGACGCTCAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4325

QY 993 AGGACTGAG 1052  
DB 4326 AGGACTGAG 4385

QY 1053 GAGCAG 1112  
DB 4386 GAGCAG 4445

QY 1113 GGTGGGTTTCCCCC-TTATAGATGCTACGACCTGGGTGTTACAAAGTTGATGTG 1171  
DB 4446 GGTGGGTTTCCCCC-TTATAGATGCTACGACCTGGGTGTTACAAAGTTGATGTG 4505

QY 1172 GCATGATATCTTCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1231  
DB 4506 GCATGATATCTTCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4565

QY 1232 AATGAGCTTCTATCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1291  
DB 4566 AATGAGCTTCTATCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4625

QY 1292 AATTAATAATATTCATGAGAA 1311  
DB 4626 NATTAANAATATTCANAGGA 4645

RESULT 12  
AX237345/c

LOCUS AX237345 285 bp DNA linear PAT 26-SEP-2001  
DEFINITION Sequence 321 from Patent WO0164886.  
ACCESSION AX237345  
VERSION AX237345.1 GI:15796899  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Homosapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
1 Gaiger, A., Algate, P. A. and Mannion, J.  
Compositions and methods for the detection, diagnosis and therapy  
of hematological malignancies  
Patent: WO 0164886-A 321 07-SEP-2001;  
CORIXA CORPORATION (US)  
location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 4.1e-68;  
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 682 CTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 741  
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QY 742 TGTGACACCCACTGACCTGCTGTAACCTTGTGAGAACACAGCCGATTCACCTGAGCAGG 801  
DB 225 TGTGACACCCACTGACCTGCTGTAACCTTGTGAGAACACAGCCGATTCACCTGAGCAGG 166

QY 802 ACCTGTAACCCCTGAGACAGAGTGTCTACATGATGATGATGATGATGATGATGATGATGATG 861  
DB 165 ACCTGTAACCCCTGAGACAGAGTGTCTACATGATGATGATGATGATGATGATGATGATGATG 106

QY 862 GCAAGAGCTGCTGCGGTAAACAGCCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 921  
DB 105 GCAAGAGCTGCTGCGGTAAACAGCCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 46

QY 922 AAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 966  
DB 45 AAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1

RESULT 13  
AX237492/c 285 bp DNA linear PAT 26-SEP-2001  
DEFINITION Sequence 468 from Patent WO0164886.  
ACCESSION AX237492  
VERSION AX237492.1 GI:15797046  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Homosapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
1 Gaiger, A., Algate, P. A. and Mannion, J.  
Compositions and methods for the detection, diagnosis and therapy  
of hematological malignancies  
Patent: WO 0164886-A 468 07-SEP-2001;  
CORIXA CORPORATION (US)  
location/Qualifiers  
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ORIGIN

Query Match 21.5%; Score 285; DB 6; Length 285;  
Best Local Similarity 100.0%; Pred. No. 4.1e-68;

Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 285 CTGAGTGAATGCTTCAAGCTCTTTCTGTCCCTTCTGTCCCTCACAAGCACTAGTATTCA 226  
QY 742 TGTTCACACCCACTCAGCTCCGTGAACCTTGAGAACACAGCCGATTCACCTGAGCAG 801  
DB 225 TGTTCACACCCACTCAGCTCCGTGAACCTTGAGAACACAGCCGATTCACCTGAGCAG 166  
QY 802 ACCTTGAACCCCTGAGACAGTGTCTCATATGTGTCTAGCGCTGATGATAACAGCGCT 861  
DB 165 ACCTTGAACCCCTGAGACAGTGTCTCATATGTGTCTAGCGCTGATGATAACAGCGCT 106  
QY 862 GCAAAAGCTGCTGCGGTAAACAGCCCTGCAAGAGCTGCGCTGTAACAGCGCTGC 921  
DB 105 GCAAAAGCTGCTGCGGTAAACAGCCCTGCAAGAGCTGCGCTGTAACAGCGCTGC 46  
QY 922 AAACGCTGCTGCCACACAGGTTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 966  
DB 45 AAACGCTGCTGCCACACAGGTTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 1

RESULT 14  
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LOCUS AX237442 285 bp DNA linear PAT 26-SEP-2001  
DEFINITION Sequence 418 from Patent WO0164886.  
ACCESSION AX237442  
VERSION AX237442.1 GI:15796996  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS 1  
TITLE Gaiger, A., Algate, P. A. and Mannion, J.  
JOURNAL Compositions and methods for the detection, diagnosis and therapy  
of hemetological malignancies  
Patent: WO 0164886-A 418 07-SEP-2001;  
CORIXA CORPORATION (US)  
FEATURES  
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Location/Qualifiers  
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Query Match 21.4%; Score 283.4; DB 6; Length 285;  
Best Local Similarity 99.6%; Pred. No. 1,1e-67;  
Matches 284; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 682 CTGAGTGAATGCTTCAAGCTCTTTCTGTCCCTTCTGTCCCTCACAAGCACTAGTATTCA 741  
DB 285 CTGAGTGAATGCTTCAAGCTCTTTCTGTCCCTTCTGTCCCTCACAAGCACTAGTATTCA 226  
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QY 862 GCAAAAGCTGCTGCGGTAAACAGCCCTGCAAGAGCTGCGCTGTAACAGCGCTGC 921  
DB 105 GCAAAAGCTGCTGCGGTAAACAGCCCTGCAAGAGCTGCGCTGTAACAGCGCTGC 46  
QY 922 AAACGCTGCTGCCACACAGGTTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 966  
DB 45 AAACGCTGCTGCCACACAGGTTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 1

RESULT 15

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LOCUS AX237542 285 bp DNA linear PAT 26-SEP-2001  
DEFINITION Sequence 518 from Patent WO0164886.  
ACCESSION AX237542  
VERSION AX237542.1 GI:15797096  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS 1  
TITLE Gaiger, A., Algate, P. A. and Mannion, J.  
JOURNAL Compositions and methods for the detection, diagnosis and therapy  
of hemetological malignancies  
Patent: WO 0164886-A 518 07-SEP-2001;  
CORIXA CORPORATION (US)  
FEATURES  
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Location/Qualifiers  
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ORIGIN

Query Match 21.4%; Score 283.4; DB 6; Length 285;  
Best Local Similarity 99.6%; Pred. No. 1,1e-67;  
Matches 284; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 682 CTGAGTGAATGCTTCAAGCTCTTTCTGTCCCTTCTGTCCCTCACAAGCACTAGTATTCA 741  
DB 285 CTGAGTGAATGCTTCAAGCTCTTTCTGTCCCTTCTGTCCCTCACAAGCACTAGTATTCA 226  
QY 742 TGTTCACACCCACTCAGCTCCGTGAACCTTGAGAACACAGCCGATTCACCTGAGCAG 801  
DB 225 TGTTCACACCCACTCAGCTCCGTGAACCTTGAGAACACAGCCGATTCACCTGAGCAG 166  
QY 802 ACCTTGAACCCCTGAGACAGTGTCTCATATGTGTCTAGCGCTGATGATAACAGCGCT 861  
DB 165 ACCTTGAACCCCTGAGACAGTGTCTCATATGTGTCTAGCGCTGATGATAACAGCGCT 106  
QY 862 GCAAAAGCTGCTGCGGTAAACAGCCCTGCAAGAGCTGCGCTGTAACAGCGCTGC 921  
DB 105 GCAAAAGCTGCTGCGGTAAACAGCCCTGCAAGAGCTGCGCTGTAACAGCGCTGC 46  
QY 922 AAACGCTGCTGCCACACAGGTTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 966  
DB 45 AAACGCTGCTGCCACACAGGTTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 1

Search completed: June 17, 2004, 13:09:49  
Job time : 5332 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 17, 2004, 14:12:51 ; Search time 65 seconds

(without alignments)  
546.516 Million cell updates/sec

Title: US-09-441-242A-2

Perfect score: 612  
Sequence: 1 AECPTLGEAVYDHPDRLMAW.....VYHIKIDGVEDMLLELPDD 113

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL 25: \*  
1: sp\_archaea: \*  
2: sp\_bacteria: \*  
3: sp\_fungi: \*  
4: sp\_human: \*  
5: sp\_invertebrate: \*  
6: sp\_mammal: \*  
7: sp\_mhc: \*  
8: sp\_organelle: \*  
9: sp\_phage: \*  
10: sp\_plant: \*  
11: sp\_rodent: \*  
12: sp\_virus: \*  
13: sp\_vertebrate: \*  
14: sp\_unclassified: \*  
15: sp\_virus: \*  
16: sp\_bacteriap: \*  
17: sp\_archaeap: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	159	26.0	33	4 Q969P8	Q969P8 homo sapien
2	148	24.2	128	4 Q9UBQ4	Q9UBQ4 homo sapien
3	86	14.1	16	Q8XEX4	Q8XEX4 salmonella
4	84.5	13.8	107	11 Q9QXN9	Q9QXN9 mus musculus
5	83	13.6	619	16 Q8XW3	Q8XW3 escherichia
6	83	13.6	620	16 Q8FDM3	Q8FDM3 escherichia
7	75.5	12.3	4099	10 Q9C726	Q9C726 arabidopsis
8	74	12.1	363	16 Q9PJ22	Q9PJ22 chlamydia m
9	73.5	12.0	196	17 P73727	P73727 synechocyst
10	73.5	12.0	931	2 Q7WY21	Q7WY21 aeropyrum p
11	73.5	12.0	931	2 Q7WY21	Q7WY21 pseudomonas
12	71.5	11.7	727	17 Q58935	Q58935 pyrococcus
13	71.5	11.7	1156	17 Q8TK58	Q8TK58 methanosaarc
14	71	11.6	380	2 Q8VVI0	Q8VVI0 erwinia pyr
15	69	11.3	363	2 Q8VRP6	Q8VRP6 desulfocell
16	69	11.3	495	3 Q96VP7	Q96VP7 pichia angu

17	69	11.3	524	11 Q80UE9	Q80UE9 mus musculus
18	69	11.3	525	11 Q80VZ4	Q80VZ4 mus musculus
19	69	11.3	574	16 Q7UV67	Q7UV67 rhodospirell
20	69	11.3	592	16 Q8RSU6	Q8RSU6 thermotaneer
21	69	11.3	603	10 Q94E86	Q94E86 oryza sativ
22	68.5	11.2	236	9 Q9G0A6	Q9G0A6 vibrio phag
23	68.5	11.2	319	3 Q9HEC8	Q9HEC8 neurospora
24	68.5	11.2	689	16 Q8FIC7	Q8FIC7 corynebacte
25	68	11.1	213	16 Q8NRD2	Q8NRD2 corynebacte
26	68	11.1	308	5 Q9V8W5	Q9V8W5 diosiphila
27	68	11.1	550	5 Q8WQ59	Q8WQ59 trichinella
28	68	11.1	1111	16 Q8IDB8	Q8IDB8 bacillus ce
29	67.5	11.0	245	16 Q7UEF8	Q7UEF8 rhodospirell
30	67.5	11.0	792	10 Q84PB3	Q84PB3 oryza sativ
31	67.5	11.0	1261	16 Q7URK6	Q7URK6 rhodospirell
32	67	10.9	236	9 Q9G0A3	Q9G0A3 vibrio phag
33	67	10.9	236	9 Q9G0A7	Q9G0A7 vibrio phag
34	67	10.9	236	9 Q9FZQ3	Q9FZQ3 vibrio phag
35	67	10.9	282	6 Q866D8	Q866D8 callichris
36	67	10.9	285	6 Q866D7	Q866D7 callichris
37	67	10.9	323	2 Q918F5	Q918F5 vibrio mimi
38	67	10.9	345	6 Q9N269	Q9N269 callichris
39	67	10.9	365	6 Q866D9	Q866D9 callichris
40	67	10.9	365	6 Q866D6	Q866D6 leontopithe
41	67	10.9	508	4 Q9NMR4	Q9NMR4 homo sapien
42	67	10.9	629	4 Q9NXG4	Q9NXG4 homo sapien
43	67	10.9	778	4 Q9BVF1	Q9BVF1 homo sapien
44	67	10.9	882	11 Q8BKJ9	Q8BKJ9 mus musculus
45	67	10.9	1054	16 Q89VP8	Q89VP8 bradyrhizob

## ALIGNMENTS

RESULT 1				
ID	Q969P8	PRELIMINARY:	PRT:	33 AA.
AC	Q969P8:			
DT	01-DEC-2001 (TREMBlrel. 19, Created)			
DT	01-DEC-2001 (TREMBlrel. 19, Last sequence update)			
DT	01-OCT-2003 (TREMBlrel. 25, Last annotation update)			
DE	Similar to T-cell leukemia/lymphoma 1A (Fragment).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX	NCBI_Taxid=9606;			
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RP	SEQUENCE FROM N.A.			
RC	TISSUE=B-cell;			
RA	Strausberg R.;			
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC009502; AA09502.1; -			
DR	EMBL; BC009891; AA09891.1; -			
DR	InterPro; IPR004832; TC1_MTC1.			
DR	Pfam; PF01840; TC1_MTC1.1.			
DR	ProDom; PD015575; TC1B.1.			
FT	NON TER			
FT	1			
SQ	SEQUENCE 33 AA; 3834 MW; 9C79E571A6C7EEFA CRC64;			
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Best Local Similarity 26.0%; Score 159; DB 4; Length 33;				
Matches 31; Conservative 96.9%; Pred. No. 1.1e-10;				
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
QY	82 RYRSSDSSFWRLVYHIKIDGVEDMLLELPDD 113			
DB	2 RGRSSDSSFWRLVYHIKIDGVEDMLLELPDD 33			
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ID	Q9UBQ4	PRELIMINARY:	PRT:	128 AA.
AC	Q9UBQ4:			
DT	01-MAY-2000 (TREMBlrel. 13, Created)			

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DT 01-MAY-2000 (TREMblrel. 13, last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, last annotation update)
DE TCU1 / MTCPI-like 1.
GN TML1.
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99274532; PubMed=10344735;
RA Sugimoto J., Hatakeyama T., Narducci M.G., Russo G., Isobe M.;
RT "Identification of the TCU1 / MTCPI-like 1 (TML1) gene from the region
RL next to the TCU1 locus.";
RN [2]
RP SEQUENCE FROM N.A.
RX TISUS-lymph;
MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Dichtenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunatirne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hallyk S.W.,
RA Villalón D.K., Mazny D.M., Sodergren E.O., Lu X., Gibbs R.A.,
RA Paley J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,
RA Jones S.J., Mair M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RN [3]
RP Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX TISUS-lymph;
RA Strausberg R.;
RL Submitted (Apr-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB025274; BAA82476.1; -.
DR EMBL; AB025272; BAA82476.1; JOINED.
DR EMBL; AB025273; BAA82476.1; JOINED.
DR EMBL; AB018563; BAA76712.1; -.
DR EMBL; BC051000; AAH51000.1; -.
DR HSSP; P56278; 1A1X.
DR InterPro; IPR004832; TCU1_MTCPI.
DR Pfam; PF01840; TCU1_MTCPI.1.
DR ProDom; PD015575; TCU1B; 1.
SQ SEQUENCE 128 AA; 1485 MW; 6BA2CF22F62CFB4D CRC64;

Query Match 24.2%; Score 148; DB 4; Length 128;
Best Local Similarity 29.2%; Pred. No. 9.3e-09;
Matches 33; Conservative 21; Mismatches 45; Indels 14; Gaps 1;

QY 14 PDRLMAWEKRYVDEKQHWLPLTEIKDLQ-----LRVLREDDVVLGR 59
DB 13 PGRMWRPGVIEDEBGRVTVVVRNPSRRREWARASQGRYEPSTVHLQWAVHTRE 72

QY 60 PMPTQTQIGPSLLPIMQLYPDGRYRSSDSSFWRLVYAIKIDGVDMLELPPD 112
DB 73 LLSGGQWPSQGLPRAVWQVLPFRKTRADSSFWELADHGQIDSMQVLTYPQE 125

RESULT 3
Q8XEX4 PRELIMINARY; PRT; 618 AA.
AC Q8XEX4;
DT 01-MAR-2002 (TREMblrel. 20, Created)

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DT 01-MAR-2002 (TREMblrel. 20, last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, last annotation update)
DE Glutathionylispermidine synthetase (Bifunctional;
DE glutathionylispermidine synthetase, glutathionylispermidine
DE amidase).
GN GSP OR T3060 OR STM3139 OR STY3310.
OS Salmonella typhi, and
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601, 602;
RN [1]
RP SEQUENCE FROM N.A.
RX SPECIES-S.typhi; STRAIN=Ty2 / ATCC 700931;
MEDLINE=2251367; PubMed=12644504;
RA Deng W., Lion S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodoyanni V., Schwartz D.C., Blatter F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RL and CT18.";
RN [2]
RP J. Bacteriol. 185:2330-2337(2003).
RN [2]
RP SEQUENCE FROM N.A.
RX SPECIES-S.typhimurium; STRAIN=L72 / SSGC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulyanay E.,
RA Ryan B., Sun H., Floria L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RL L72.";
RN [3]
RP Nature 413:852-856(2001).
RN [3]
RP SEQUENCE FROM N.A.
RX SPECIES-S.typhi; STRAIN=CT18;
MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Main J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebatia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Felwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagsels K.,
RA Krogan A., Larsen T.S., Leather S., Moule S., O'Garra P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrett B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RL enterica serovar Typhi CT18.";
RN [4]
RP Nature 413:848-852(2001).
DR EMBL; AE016844; AA070606.1; -.
DR EMBL; AE008844; AAL22013.1; -.
DR EMBL; AL627277; CAD02971.1; -.
DR InterPro; IPR007921; CHAP.
DR InterPro; IPR005484; GSP_synth.
DR Pfam; PF05257; CHAP; 1.
DR Pfam; PF03738; GSP_synth; 1.
DR PROSITE; PS50911; CHAP; 1.
KW Complete proteome.
SQ SEQUENCE 618 AA; 70240 MW; E24F56812160EC60 CRC64;

Query Match 14.1%; Score 86; DB 16; Length 618;
Best Local Similarity 29.7%; Pred. No. 0.59;
Matches 22; Conservative 20; Mismatches 26; Indels 6; Gaps 3;

QY 16 RLMAW-----EKFVYDEKQHWLPLTEIKDLQRLVLREDDVVLGRPM--TPQIGPS 69
DB 433 KTWAMETAMEQIREVSETEIYAVPIRTGHPENVRLLIDVLRPEVLFEPMTVLPNGKA 498

QY 70 LPLIMQLYPDGRY 83
DB 499 ILPLMSLPFHRY 512

RESULT 4
Q9QXN9

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RESULT 7
O9C726 PRELIMINARY; PRT; 4099 AA.
ID O9C726
AC O9C726
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.
GN T2015.2.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Eusterois II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Elgu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gili J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huitzar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremetska I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Matzliak A.,
RA Miltner J., Miranda M., Nguyen M., Niernan W.C., Osborne B.T.,
RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Uterback T., Van Aken S., Vaysberg M., Vysotska V.S., Walker M.,
RA Wu D., Xu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT thaliana."
RL Nature 408:816-820(2000).
CC -1 SIMILARITY: CONTAINS 1 C2 DOMAIN.
DR EMBL; AC051631; AAG51531.1; -
DR InterPro; IPR000008; C2.
DR Pfam; PF00168; C2; 1.
DR SMART; SM00239; C2; 1.
DR PROSITE; PS50004; C2_DOMAIN_2; 1.
KM Hypothetical protein.
SQ SEQUENCE 4099 AA; 456577 MW; EA3PD90A5C4FB85 CRC64;

Query Match 12.3%; Score 75.5; DB 10; Length 4099;
Best Local Similarity 22.7%; Pred. No. 87;
Matches 25; Conservative 18; Mismatches 28; Indels 39; Gaps 5;

QY 27 DEKQAWLPTLTIKRLQLRLRREDVVLGRPMTPQIGPSL-----LPIW 75
DB 356 EEQYHDIKL-VEVVSRYKTYI-----FISHLRNVVSEVPRKMWPPAQAASIQQRLL 409
QY 76 -----QIYPDGRYSSDSF-----WRIVYHIKIDGVE 103
DB 410 YTRYIQYANFLQSSDVNYPEMREIKMDLSKVILLRLLAAKVESVK 459

RESULT 8
O9PU22 PRELIMINARY; PRT; 275 AA.
ID O9PU22
AC O9PU22
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Hypothetical protein TC0684.
GN TC0684.
OS Chlamydia muridarum.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83560;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=MoBn / Nigg;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brumham R.C., Shen C., Gili S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Uterback T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwin M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoBn and Chlamydia
RT pneumoniae AR39."
RL Nucleic Acids Res. 28:1397-1406(2000).
DR EMBL; AE002337; AAF39501.1; -
DR PIR; F81675; F81675.
DR TIGR; TC0684; -
KM Hypothetical protein; Complete proteome.
SQ SEQUENCE 275 AA; 31234 MW; 591AB4376AB83A49 CRC64;

Query Match 12.3%; Score 75; DB 16; Length 275;
Best Local Similarity 33.7%; Pred. No. 3.9;
Matches 28; Conservative 10; Mismatches 29; Indels 16; Gaps 4;

QY 39 EICDRLQLRLRREDVVLGRPMTPQIGPSLPIWQLYP-----DGRYSSDS 88
DB 5 ELDSGDKKLERFKXVILIRP-SATAIWPKTSPALMKQYSAFVVGKGEKWKYNSHL 63
QY 89 SFWRIVYHIKIDGVEMLLELP 111
DB 64 KEM-----WITIDSV-SCLKLTP 81

RESULT 9
P73727 PRELIMINARY; PRT; 363 AA.
ID P73727
AC P73727
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Hypothetical protein slr1737.
GN slr1737.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hikosawa M., Sugita M., Sasaoka S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naito K., Okumura S.,
RA Shimo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions."
RL DNA Res. 3:109-136(1996).
DR EMBL; D90909; BAA17775.1; -
DR PIR; S74814; S74814.
KM Hypothetical protein; Complete proteome.
SQ SEQUENCE 363 AA; 41479 MW; 992646CFD296D35 CRC64;

Query Match 12.1%; Score 74; DB 16; Length 363;
Best Local Similarity 25.0%; Pred. No. 7;
Matches 26; Conservative 15; Mismatches 31; Indels 32; Gaps 6;

QY 14 PDLRAWKRFVYLDEKQAWLPLTTEIKRLQLRLRREDVVLGRPMTP----- 64
DB 211 PSR-WFWLDQANYPD--HPGLSVTAAGGR-----IVLRPERVALIGLHQGN 256
QY 65 --QIGPSLPIWQLYPDGRY--RSSDSFWRIVYHIKIDGVE 104
DB 257 FYEFGHGCTVTVQVAPKGRMQLKASNDRYW-----VLDSGXTD 295

RESULT 10
O9YB77

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ID Q9YB77 PRELIMINARY; PRT; 196 AA.
AC Q9YB77;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 196AA long hypothetical cytochrome oxidase subunit II.
GN APEI720.
OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcaceae;
OC Desulfurococcaceae; Aeropyrum.
OX NCBI_TaxID=56536;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K1;
RX MEDLINE=99310339; PubMed=10382966;
RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Anaki A., Kosugi H.,
RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
RA Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
RA Nakamura Y., Nomura N., Sake Y., Kikuchi H.,
RT "Complete genome sequence of an aerobic hyper-thermophilic
RT crenarchaeon, Aeropyrum pernix K1."
RL DNA Res. 6:83-101(1999).
DR EMBL; AP000062; BAA80721.1; -.
DR PIR; D72554; D72554.
DR HSSP; P98052; 2CUN.
DR GO; GO:0005507; F:copper ion binding; IEA.
DR InterPro; IPR001505; Copper_Gua.
DR InterPro; IPR008972; Cupredoxin.
DR ProDom; PD000131; Copper_Gua; 1.
DR PROSITE; PS00078; COX2; 1.
SK Complete proteome.
SQ SEQUENCE 196 AA; 21524 MW; 9E0374DEDEBDB164 CRC64;

Query Match
Beet Local Similarity 27.5%; Score 73.5; DB 17; Length 196;
Matches 19; Conservative 13; Mismatches 26; Indels 11; Gaps 3;

QY 24 VYLDKQAHMLPTTEIKRDLRLVLRREDVVLGRPMPTPTQIGPSLFP-----IMWOLY 78
DB 72 VYIVROFVWIPSTIVLEDPKQVTFVATSDVIHGFELIGTVNFMVIFGYIAKFTW--Y 129
QY 79 P-----DGRY 83
DB 130 PPKNAAGEY 138

RESULT 11
Q7WY21 PRELIMINARY; PRT; 931 AA.
AC Q7WY21;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Kinase sensor protein of two component regulatory system.
GN RL036.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PA14;
RA He J., Rahme L.G.;
RT "Pseudomonas aeruginosa PA14 pathogenicity island (PAI) 1."
RT Submitted (Apr-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY273869; AAP84163.1; -.
KW Kinase.
SQ SEQUENCE 931 AA; 101651 MW; C49570546B3B3141 CRC64;

Query Match
Beet Local Similarity 12.0%; Score 73.5; DB 2; Length 931;
Matches 30.2%; Pred. No. 25;

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Matches 39; Conservative 10; Mismatches 43; Indels 37; Gaps 7;

QY 10 VTD--HPRILNAKEFVYLDKQAHMLPTTEIKRDLRLVLRREDVVLGRPMPTPTQIG 67
DB 177 VTDGTFPRQLVLFELG--DEPGEGWGLLEIIGED---LDSMLRNDA--GNYMLDQHG 229
QY 68 PSLPIPMQLYPDGYS-----SDSSFMVLVHIKIDGYE 103
DB 220 QVVLATDVALGSGASRTILRGDGRFGIAGPLPQHMYLPQHVHSSSMDLIYHI---GIG 286
QY 104 DMLLEL-LP 111
DB 287 RLILALMLP 295

RESULT 12
OS8935
ID 058935 PRELIMINARY; PRT; 727 AA.
AC 058935;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein PH1246.
GN PH1246.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococci; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=53953;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OT3;
RX MEDLINE=98344137; PubMed=9679194;
RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohtuku Y.,
RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3."
RL DNA Res. 5:55-76(1998).
CC -1 SIMILARITY: TO DEAD/DEAH BOX HELICASE FAMILY.
DR EMBL; AP000005; BAA30347.1; -.
DR PIR; A71069; A71069.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008026; F:ATP dependent helicase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR006474; Cas3 core.
DR InterPro; IPR006483; CRISPR_HD.
DR InterPro; IPR01410; DEAD.
DR InterPro; IPR001650; Helicase_C.
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF00271; Helicase_C; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
DR TIGRfams; TIGR01587; cas3_core; 1.
DR TIGRfams; TIGR01596; cas3_HD; 1.
DR ATP-binding; Helicase; Hypothetical protein; Complete proteome.
SQ SEQUENCE 727 AA; 84768 MW; 6AAFD011AD2FDC5 CRC64;

Query Match
Beet Local Similarity 11.7%; Score 71.5; DB 17; Length 727;
Matches 26; Conservative 13; Mismatches 42; Indels 13; Gaps 3;

QY 21 EKFYVLDKQAHMLPTTEIKRDLRLVLRREDVVLGRPMPTPTQIGPSLPIPMQLYPD 80
DB 221 EQFVEMKIPREKMR-----LQLSSSMTEGCVITL---YAPTYGKTEAALLNANKNA 269
QY 81 GRYSSDS--FMRLVHIKIDGVEDMLLELPP 112
DB 270 HRTKGISRIFYILPYKASINAMHRLLEMKD 303

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RESULT 13
O8TK58      PRELIMINARY;      PRT;      1156 AA.
AC      O8TK58;
DT      01-JUN-2002 (TREMBlrel. 21, Created)
DT      01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT      01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE      Phosphorylase.
GN      MA3560.
OS      Methanosarcina acetivorans.
OC      Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
OC      Methanosarcinales; Methanosarcinaceae; Methanosarcina.
OX      NCBI_TaxID=2214;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C2A / ATCC 35395 / DSM 2834;
RX      MEDLINE=21929760; PubMed=11932238;
RA      Galagan J.E., Nuebaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA      Fitzhugh W., Calvo S., Engels R., Smirnov S., Alnoor D., Brown A.,
RA      Allen N., Naylor J., Stange-Thomann N., Deatellano K., Johnson R.,
RA      Linton L., McMan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA      Zimmer A., Barber R.D., Cann I., Graham D.E., Grathame D.A., Gues A.M.,
RA      Hedderich R., Ingram-Smith C., Kuetner H.C., Krzycki J.A.,
RA      Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA      Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
RA      Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA      Mercalf W.W., Birren B.;
RT      "The genome of Methanosarcina acetivorans reveals extensive metabolic
RT      and physiological diversity."
RL      Genome Res. 12:532-542(2002).
DR      EMBL; AB011064; AAM0921.1; -.
DR      GO; GO:0003824; F:catalytic activity; IEA.
DR      GO; GO:0009116; P:nucleoside metabolism; IEA.
DR      InterPro; IPR008938; ARM.
DR      InterPro; IPR00845; FNP_UDP.
DR      Pfam; PF01048; FNP_UDP_1; 1.
KW      Complete proteome.
SQ      SEQUENCE 1156 AA; 130192 MW; 0280A362DC4B5C6 CRC64;

Query Match      11.7%; Score 71.5; DB 17; Length 1156;
Best Local Similarity 23.0%; Pred. No. 54;
Matches 26; Conservative 20; Mismatches 42; Indels 25; Gaps 5;

QY      6 LGAAVTDHPDRLMAWEKFFVYLDKQKAWLPLTI-----ETKDRLOQ---RVLRLR 52
DB      494 LGSAFSGVDPDKQASMSNIKISTBEDNMKRSAYFALGASQVDPDKQASMDIRGLTIN 553
QY      53 EDVVLGRMPPTQIGPSILPLTMQLYPDGRYSSDSFMRVLVYHIKIDGVEDM 105
DB      554 EDSVY-RRITASALGSAFSHV-----PD-----KQKAMNDLHRLSIDKEDV 594

RESULT 14
O8VVI0      PRELIMINARY;      PRT;      380 AA.
AC      O8VVI0;
DT      01-MAR-2002 (TREMBlrel. 20, Created)
DT      01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT      01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE      Membrane protein.
GN      CPSH.
OS      Erwinia pyrifoliae.
OC      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC      Enterobacteriaceae; Erwinia.
OX      NCBI_TaxID=79967;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Epl/96;
RA      Kim W.S., Schollmeyer M., Nimetz M., Geider K.;
RT      "Structural and molecular properties of the capsular exopolysaccharide
RT      from the Asian pear pathogen Erwinia pyrifoliae."
RL      Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.

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DR      EMBL; AJ300463; CAC82927.1; -.
DR      GO; GO:0016020; C:membrane; IEA.
DR      GO; GO:0015159; F:polysaccharide transporter activity; IEA.
DR      GO; GO:0015774; P:polysaccharide transport; IEA.
DR      InterPro; IPR003715; Poly_export.
DR      Pfam; PF02563; Poly_export; 1.
SQ      SEQUENCE 380 AA; 42023 MW; BC4C5A0A7EC66E8C CRC64;

Query Match      11.6%; Score 71; DB 2; Length 380;
Best Local Similarity 24.0%; Pred. No. 16;
Matches 23; Conservative 23; Mismatches 34; Indels 16; Gaps 4;

QY      5 TLGAAYTDHPDRLMAWEKFFVYLDKQKAWLPLTIETIKRLQLRLRREDVVLGRMPPT 64
DB      34 TMGKDVVEQDSDPDIDKYVNV-----FPLTSLVERKRPVVAQANATLQRELQNY 86
QY      65 Q----IGPSILPLTMQ---LYPDGRYRS-SDSSF 91
DB      87 EYRIGVDVLMVTVMWHPDLTPAGQYRSASDTGNW 122

RESULT 15
O8VRP6      PRELIMINARY;      PRT;      363 AA.
AC      O8VRP6;
DT      01-MAR-2002 (TREMBlrel. 20, Created)
DT      01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT      01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE      Dissimilatory sulfate reductase alpha subunit (Fragment).
GN      DSR4.
OS      Desulfocella halophila.
OC      Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacteriales;
OC      Desulfobacteriaceae; Desulfocella.
OX      NCBI_TaxID=66835;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=DSM 11763;
RX      MEDLINE=21617390; PubMed=11741869;
RA      Friedrich M.W.;
RT      "Phylogenetic Analysis Reveals Multiple Lateral Transfers of
RT      Adenosine-5'-Phosphosulfate Reductase Genes among Sulfate-Reducing
RT      Microorganisms."
RL      J. Bacteriol. 184:278-289(2002).
DR      EMBL; AF418200; AAL57473.1; -.
DR      GO; GO:0006118; P:electron transport; IEA.
DR      InterPro; IPR006067; Nir_Str_4Fe4S.
DR      Pfam; PF01077; Nir_Str; 1.
FT      NON_TER 1
SQ      SEQUENCE 363 AA; 41462 MW; 76D24998C7B1589A CRC64;

Query Match      11.3%; Score 69; DB 2; Length 363;
Best Local Similarity 24.7%; Pred. No. 26;
Matches 22; Conservative 16; Mismatches 19; Indels 32; Gaps 4;

QY      8 EAVTDHPDRLMAWEKFFVYLDKQKAWLPLTIETIKRLQLRLRREDVVLGRMPPTQIG 67
DB      282 EATIDYIDIKIMW-----WM---MEGKNNRRLGELIRQ-----G 313
QY      68 PSLLPLTMQLYPDGRY-----RSSDSFMR 92
DB      314 PQKMLEMCEVDPDPRHVAYPRENPYIFWK 342

Search completed: June 17, 2004, 14:27:59
Job time : 67 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 17, 2004, 11:31:10 ; Search time 614 Seconds  
(without alignments)  
9878.440 Million cell updates/sec

Title: US-09-441-242a-1  
Perfect score: 1324  
Sequence: 1 ctctgagagcctcgcctctt.....catcgaaaaaaaaaaaaaa 1324

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3017426 seqs, 2290544650 residues

Total number of hits satisfying chosen parameters: 6034852

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_NA:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*
- 6: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*
- 17: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 18: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 19: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1324	100.0	1324	9	US-09-796-692-665
2	1324	100.0	1324	15	US-10-040-862-665
3	1324	100.0	1324	15	US-10-171-581-925
4	1324	100.0	1324	16	US-10-057-475B-665
5	1324	100.0	1324	16	US-10-154-884B-665
6	1280	96.7	1368	15	US-10-037-270-871
7	1280	96.7	1368	16	US-10-117-722-871
8	344	26.0	369	16	US-10-057-475B-10484
9	344	26.0	369	16	US-10-154-884B-10484
10	285	21.5	285	9	US-09-796-692-321
11	285	21.5	285	9	US-09-796-692-468
12	285	21.5	285	9	US-09-796-692-3032
13	285	21.5	285	9	US-09-796-692-5832
14	285	21.5	285	9	US-09-796-692-6894

C 15	285	21.5	285	15	US-10-040-862-321	Sequence 321, App
C 16	285	21.5	285	15	US-10-040-862-468	Sequence 468, App
C 17	285	21.5	285	15	US-10-040-862-3032	Sequence 3032, App
C 18	285	21.5	285	15	US-10-040-862-5832	Sequence 5832, App
C 19	285	21.5	285	15	US-10-040-862-6894	Sequence 6894, App
C 20	285	21.5	285	16	US-10-057-475B-321	Sequence 321, App
C 21	285	21.5	285	16	US-10-057-475B-468	Sequence 468, App
C 22	285	21.5	285	16	US-10-057-475B-3032	Sequence 3032, App
C 23	285	21.5	285	16	US-10-057-475B-5832	Sequence 5832, App
C 24	285	21.5	285	16	US-10-057-475B-6894	Sequence 6894, App
C 25	285	21.5	285	16	US-10-154-884B-321	Sequence 321, App
C 26	285	21.5	285	16	US-10-154-884B-468	Sequence 468, App
C 27	285	21.5	285	16	US-10-154-884B-3032	Sequence 3032, App
C 28	285	21.5	285	16	US-10-154-884B-5832	Sequence 5832, App
C 29	285	21.5	285	16	US-10-154-884B-6894	Sequence 6894, App
C 30	284.4	21.5	290	9	US-09-796-692-6197	Sequence 6197, App
C 31	284.4	21.5	290	15	US-10-040-862-6197	Sequence 6197, App
C 32	284.4	21.5	290	16	US-10-057-475B-6197	Sequence 6197, App
C 33	284.4	21.5	290	16	US-10-154-884B-6197	Sequence 6197, App
C 34	283.4	21.4	285	9	US-09-796-692-418	Sequence 418, App
C 35	283.4	21.4	285	9	US-09-796-692-518	Sequence 518, App
C 36	283.4	21.4	285	9	US-09-796-692-6556	Sequence 6556, App
C 37	283.4	21.4	285	15	US-10-040-862-418	Sequence 418, App
C 38	283.4	21.4	285	15	US-10-040-862-518	Sequence 518, App
C 39	283.4	21.4	285	15	US-10-040-862-6556	Sequence 6556, App
C 40	283.4	21.4	285	16	US-10-057-475B-418	Sequence 418, App
C 41	283.4	21.4	285	16	US-10-057-475B-518	Sequence 518, App
C 42	283.4	21.4	285	16	US-10-057-475B-6556	Sequence 6556, App
C 43	283.4	21.4	285	16	US-10-154-884B-418	Sequence 418, App
C 44	283.4	21.4	285	16	US-10-154-884B-518	Sequence 518, App
C 45	283.4	21.4	285	16	US-10-154-884B-6556	Sequence 6556, App

## ALIGNMENTS

RESULT 1  
US-09-796-692-665  
Sequence 665, Application US/09796692  
Publication No. US20020198362A1  
GENERAL INFORMATION:  
APPLICANT: Galger, Alexander  
APPLICANT: Algate, Paul A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY  
FILE REFERENCE: 2077, 001200  
CURRENT FILING DATE: 2001-03-01  
PRIOR FILING DATE: 2001-03-01  
PRIOR APPLICATION NUMBER: 60/166,126  
PRIOR FILING DATE: 2000-03-01  
PRIOR APPLICATION NUMBER: 60/190,479  
PRIOR FILING DATE: 2000-03-17  
PRIOR APPLICATION NUMBER: 60/200,545  
PRIOR FILING DATE: 2000-04-27  
PRIOR APPLICATION NUMBER: 60/200,303  
PRIOR FILING DATE: 2000-04-28  
PRIOR APPLICATION NUMBER: 60/200,779  
PRIOR FILING DATE: 2000-04-28  
PRIOR APPLICATION NUMBER: 60/200,999  
PRIOR FILING DATE: 2000-05-01  
PRIOR APPLICATION NUMBER: 60/202,084  
PRIOR FILING DATE: 2000-05-04  
PRIOR APPLICATION NUMBER: 60/206,201  
PRIOR FILING DATE: 2000-05-22  
PRIOR APPLICATION NUMBER: 60/218,950  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: 60/222,903  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: 60/223,416  
PRIOR FILING DATE: 2000-08-04  
PRIOR APPLICATION NUMBER: 60/223,378  
PRIOR FILING DATE: 2000-08-07

NUMBER OF SEQ ID NOS: 9597  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO: 665  
LENGTH: 1324  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-796-692-665

Query Match 100.0%; Score 1324; DB 9; Length 1324;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1324; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 CTGAGAGGCTCTGCTCTTCTTGAAGCGCCGAGAGCCATGAGCCGAGTGGCCG 60
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DB 61 ACACCTGGGGAGGAGTCAACCGACCCGAGCCGCTGTGGGCTTGGAGAGTTCTGT 120
QY 121 TATTGGAAGAGACAGACAGCCCTGCTGCTTAAACATTCAGATTAAGATAGTTA 180
DB 121 TATTGGAAGAGACAGACAGCCCTGCTGCTTAAACATTCAGATTAAGATAGTTA 180
QY 181 CAGTTACGGGTGCTCTTCTGCGGAGAACGTCGCTGTGGGAGGCTATGACCCCAAC 240
DB 181 CAGTTACGGGTGCTCTTCTGCGGAGAACGTCGCTGTGGGAGGCTATGACCCCAAC 240
QY 241 CAGATAGGCCCAAGCTGCTGCTATCATGTGGAGCTCTTACCTGATGACGATACCGA 300
DB 241 CAGATAGGCCCAAGCTGCTGCTATCATGTGGAGCTCTTACCTGATGACGATACCGA 300
QY 301 TCTCAGACTCCAGTTTCGAGGCTTACTGTATCAACATCAAGATTAAGCGGTGAGAGAC 360
DB 301 TCTCAGACTCCAGTTTCGAGGCTTACTGTATCAACATCAAGATTAAGCGGTGAGAGAC 360
QY 361 ATGCTTCTGAGCTGCTGCCAGATGATGATGTCTTGGAGAGCACTGTCTCTT 420
DB 361 ATGCTTCTGAGCTGCTGCCAGATGATGATGTCTTGGAGAGCACTGTCTCTT 420
QY 421 CACCCAGGGCTGAGCTGCGCAGCTTACATAGGGATGTGTGTTCTGTTCACCTTC 480
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QY 481 GTTACTATGCTGCTGTCTTCTCCACCAAGCTGGGGTCTGGAGAGAAATGACAGACAG 540
DB 481 GTTACTATGCTGCTGTCTTCTCCACCAAGCTGGGGTCTGGAGAGAAATGACAGACAG 540
QY 541 GATGAGCTCTAACCCAGGGCTTGCAGAGACTGCTGTAGCCCACTCTGCTGCTTACAC 600
DB 541 GATGAGCTCTAACCCAGGGCTTGCAGAGACTGCTGTAGCCCACTCTGCTGCTTACAC 600
QY 601 TACCACTCCCTGGCAAGAGATTCATTTGGCAGAGCTTCTTCAGAGTGCACACTATAC 660
DB 601 TACCACTCCCTGGCAAGAGATTCATTTGGCAGAGCTTCTTCAGAGTGCACACTATAC 660
QY 661 CTGAGCTCGGCTTTCTCAGCTGATGATGTCTTCAAGCTCTTCTGTCCTTCTGTC 720
DB 661 CTGAGCTCGGCTTTCTCAGCTGATGATGTCTTCAAGCTCTTCTGTCCTTCTGTC 720
QY 721 CCTACAGCACTAGTATTTCTATGTTCACACCACTGAGCTCCGTGAATTTGAGAAC 780
DB 721 CCTACAGCACTAGTATTTCTATGTTCACACCACTGAGCTCCGTGAATTTGAGAAC 780
QY 781 CAGCCGATTAACCTGAGAGAGCTCTGAAACCTTGACCAAGTGTCTCAATGTGCTTA 840
DB 781 CAGCCGATTAACCTGAGAGAGCTCTGAAACCTTGACCAAGTGTCTCAATGTGCTTA 840
QY 841 CGCCTGATGTAACAAGCTGCAAAAGCTGCTGCGGTAAACAAGCTGCAAAAGCTG 900
DB 841 CGCCTGATGTAACAAGCTGCAAAAGCTGCTGCGGTAAACAAGCTGCAAAAGCTG 900
QY 901 CTGCGCCGTAAACAAGCTGCAAAAGCTGCTGCGGTAAACAAGCTGCAAAAGCT 960
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QY 961 GAAAGCCTGAAAGAGACCCCTTATCTGTGCTCAGAGACTCAGAAAGCTTGGTCAAGGT 1020
DB 961 GAAAGCCTGAAAGAGACCCCTTATCTGTGCTCAGAGACTCAGAAAGCTTGGTCAAGGT 1020
QY 1021 CCACATCCCGGAGCGCAGCAGAGAGCCGCGGAGCCCTGTGATGATGAGCCCTCAGAA 1080
DB 1021 CCACATCCCGGAGCGCAGCAGAGAGCCGCGGAGCCCTGTGATGATGAGCCCTCAGAA 1080
QY 1081 CCCTGGCTTGGCCACGCTGGAAGAGATGAGAGTTGGTTTCCCTTATAGATGCT 1140
DB 1081 CCCTGGCTTGGCCACGCTGGAAGAGATGAGAGTTGGTTTCCCTTATAGATGCT 1140
QY 1141 CAGCAGCTGGGTGTAAACAAGTTGATGTGAGATTAATCTTTGATATGATTA 1200
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QY 1201 AATGCAAGATGTTTATCTTACTTGTGGCAATCAGCTTATCCTTGAATTGAT 1260
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QY 1261 GGTGAGAGAGTGAAGATGAGCAGCCCAATTAATATTCATGAAAAA 1320
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QY 1321 AAAA 1324
DB 1321 AAAA 1324
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RESULT 2  
US-10-040-862-665  
Sequence 665, Application US/10040862  
Publication No. US20030078396A1  
GENERAL INFORMATION:  
APPLICANT: Gaiger, Alexander  
APPLICANT: Mannon, Jane  
APPLICANT: Reller, Marc  
APPLICANT: Corixa Corporation  
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy  
FILE REFERENCE: 014058-013520US  
CURRENT APPLICATION NUMBER: US/10/040,862  
PRIOR FILING DATE: 2001-11-06  
PRIOR APPLICATION NUMBER: US 60/186,126  
PRIOR FILING DATE: 2000-03-01  
PRIOR APPLICATION NUMBER: US 60/190,479  
PRIOR FILING DATE: 2000-03-17  
PRIOR APPLICATION NUMBER: US 60/200,545  
PRIOR FILING DATE: 2000-04-27  
PRIOR APPLICATION NUMBER: US 60/200,303  
PRIOR FILING DATE: 2000-04-28  
PRIOR APPLICATION NUMBER: US 60/200,779  
PRIOR FILING DATE: 2000-04-28  
PRIOR APPLICATION NUMBER: US 60/200,999  
PRIOR FILING DATE: 2000-05-01  
PRIOR APPLICATION NUMBER: US 60/202,084  
PRIOR FILING DATE: 2000-05-04  
PRIOR APPLICATION NUMBER: US 60/206,201  
PRIOR FILING DATE: 2000-05-22  
PRIOR APPLICATION NUMBER: US 60/218,950  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 60/222,903  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: US 60/223,416  
PRIOR FILING DATE: 2000-08-04  
PRIOR APPLICATION NUMBER: US 60/223,378  
PRIOR FILING DATE: 2000-08-07  
PRIOR APPLICATION NUMBER: US 09/796,692  
PRIOR FILING DATE: 2001-03-01



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DB 181 CAGTTACGGGTCTCTTGGCTGGGAGACGTCTCTGGGAGGCTTATGACCCCAAC 240
QY 241 CAGATAGGCCCAAGCCTGCTGCTCATATGATGAGCTTACCTGATGAGATACCGA 300
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QY 301 TCCTGAGACTCCAGTTTCTGGGCTTAGTGTACCATCAATAATGAGCGCTGAGAGAC 360
DB 301 TCCTGAGACTCCAGTTTCTGGGCTTAGTGTACCATCAATAATGAGCGCTGAGAGAC 360
QY 361 ATGCTTCTGAGCTGCTGCTGAGATGATGATGATGATGATGATGATGATGATGATG 420
DB 361 ATGCTTCTGAGCTGCTGCTGAGATGATGATGATGATGATGATGATGATGATGATG 420
QY 421 CACCCAGGAGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 480
DB 421 CACCCAGGAGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 480
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DB 481 GTTACTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
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QY 661 CTGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
DB 661 CTGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
QY 721 CCTCAGACACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780
DB 721 CCTCAGACACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780
QY 781 CAGCGGATTCAGCTGAGGAGGAGCTGAGGAGGAGCTGAGGAGGAGCTGAGGAGGAG 840
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DB 841 CGCTGCTGATGTAACACGCTGCAACGCTGCAACGCTGCAACGCTGCAACGCTGCA 900
QY 901 CCTGCGCTTAAACACGCTGCAACGCTGCAACGCTGCAACGCTGCAACGCTGCAAC 960
DB 901 CCTGCGCTTAAACACGCTGCAACGCTGCAACGCTGCAACGCTGCAACGCTGCAAC 960
QY 961 GAAAGGCTGAAAGGAGGAGCTGAAAGGAGGAGCTGAAAGGAGGAGCTGAAAGGAG 1020
DB 961 GAAAGGCTGAAAGGAGGAGCTGAAAGGAGGAGCTGAAAGGAGGAGCTGAAAGGAG 1020
QY 1021 CCACATCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
DB 1021 CCACATCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
QY 1081 CCCTTGGCTTGGCCACGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
DB 1081 CCCTTGGCTTGGCCACGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
QY 1141 CAGGCACTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200
DB 1141 CAGGCACTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200
QY 1201 AATGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
DB 1201 AATGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
QY 1261 GGTGGAGAGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1320
DB 1261 GGTGGAGAGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1320
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DB 1261 GGTGGAGAGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1320
QY 1321 AAAA 1324
DB 1321 AAAA 1324

RESULT 4
US-10-057-475B-665
; Sequence 665, Application US/10057475B
; Publication No. US20040002068A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordonez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-014402US
; CURRENT APPLICATION NUMBER: US/10/057,475B
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10979
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 665
; LENGTH: 1324
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-057-475B-665

Query Match 100.0%; Score 1324; DB 16; Length 1324;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1324; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGAGAGGCTCTGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 60
DB 1 CTTGAGAGGCTCTGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 60
QY 61 ACACCTCGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120
DB 61 ACACCTCGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120
QY 121 TATTTGAGAGAGACAGACAGCGCTGCTGCTTAAACCATCGAGATTAAGATAGTTA 180
DB 121 TATTTGAGAGAGACAGACAGCGCTGCTGCTTAAACCATCGAGATTAAGATAGTTA 180
QY 181 CAGTTACGGGCTCTTCTGCTGAGAGAGGCTGCTGCTGAGGAGGCTTATGAGCCCAAC 240
DB 181 CAGTTACGGGCTCTTCTGCTGAGAGAGGCTGCTGCTGAGGAGGCTTATGAGCCCAAC 240
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Db 181 CAGTTACGGGTCCTTGGCTGGGAGACGTCCTGAGGAGGCGCTATGACCCCAACC 240
Qy 241 CAGATTAGGCCAAGCCTGCTGCTATCATGTGGAGCCTTACCTGATGAGATACGA 300
Db 241 CAGATTAGGCCAAGCCTGCTGCTATCATGTGGAGCCTTACCTGATGAGATACGA 300
Qy 301 TCCCTAGACTCCAGTTTCTGGGCTTATGTACCAATCAATGAATGACGGCGTGAGAC 360
Db 301 TCCCTAGACTCCAGTTTCTGGGCTTATGTACCAATCAATGAATGACGGCGTGAGAC 360
Qy 361 ATGCTTCTGAGCTGCTGCAATGATGATGTATGCTTGGCAGACCTGTCTCTTT 420
Db 361 ATGCTTCTGAGCTGCTGCAATGATGATGTATGCTTGGCAGACCTGTCTCTTT 420
Qy 421 CACCCAGGGGCTGAGCCTGGCAGCTTCAATGGGAGTGTGTCTGTTCACCTTC 480
Db 421 CACCCAGGGGCTGAGCCTGGCAGCTTCAATGGGAGTGTGTGTCTGTTCACCTTC 480
Qy 481 GTTTACTATGCTGTCTTCTTCCACCAAGCTGGGCTGGGAGGATGAGACAGAG 540
Db 481 GTTTACTATGCTGTCTTCTTCCACCAAGCTGGGCTGGGAGGATGAGACAGAG 540
Qy 541 GATGAGCTTACCCAGGGGCTGAGGACCTGCTGTGAGCCACTGTGCTGAGTAC 600
Db 541 GATGAGCTTACCCAGGGGCTGAGGACCTGCTGTGAGCCACTGTGCTGAGTAC 600
Qy 601 TACCACTCCTGCAAGAGAGATTTCCATTTGGCAGAGCTTCTTCCAGTGGCCAGCTATAC 660
Db 601 TACCACTCCTGCAAGAGAGATTTCCATTTGGCAGAGCTTCTTCCAGTGGCCAGCTATAC 660
Qy 661 CTGTGCTGAGCTTCTTCTGAGCTGATGATGCTTTCAGCCTCTTCTGCTCTGTC 720
Db 661 CTGTGCTGAGCTTCTTCTGAGCTGATGATGCTTTCAGCCTCTTCTGCTCTGTC 720
Qy 721 CCTCAAGACATGATTTTCACTGTGCACACCACTGAGCTCGTGAATTTGAGAAC 780
Db 721 CCTCAAGACATGATTTTCACTGTGCACACCACTGAGCTCGTGAATTTGAGAAC 780
Qy 781 CAGCCGATTCACCTGAGAGGACCTTGTAAACCTTGGACCAATGCTTCAATGTGTCTA 840
Db 781 CAGCCGATTCACCTGAGAGGACCTTGTAAACCTTGGACCAATGCTTCAATGTGTCTA 840
Qy 841 CGCCTGCAATGTAAACAGCCTGCAACAGCTGCTGCGGTAAACAGCCTGCAACAGCTG 900
Db 841 CGCCTGCAATGTAAACAGCCTGCAACAGCTGCTGCGGTAAACAGCCTGCAACAGCTG 900
Qy 901 CCTGCGCGTAAACAGCCTGCAACAGCTGCTGCGGTAAACAGCCTGCAACAGCTG 960
Db 901 CCTGCGCGTAAACAGCCTGCAACAGCTGCTGCGGTAAACAGCCTGCAACAGCTG 960
Qy 961 GAAAGGCTGAAAGAGGAGCCTTATCTGTGCTAGAGACTCAGAAAGCCTTGAGTCAGTGT 1020
Db 961 GAAAGGCTGAAAGAGGAGCCTTATCTGTGCTAGAGACTCAGAAAGCCTTGAGTCAGTGT 1020
Qy 1021 CCACATCCCGGAGCGAGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGG 1080
Db 1021 CCACATCCCGGAGCGAGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGG 1080
Qy 1081 CCTTGGCTTGGCCAGTGGAAAGAGATGAGGTTGGGTTTCCCCCTTTATAGATGT 1140
Db 1081 CCTTGGCTTGGCCAGTGGAAAGAGATGAGGTTGGGTTTCCCCCTTTATAGATGT 1140
Qy 1141 CACGCACTGGGTTGTTACAAAGTTGTATGTGCAATGAAATCTTTTGTATATGATGATTA 1200
Db 1141 CACGCACTGGGTTGTTACAAAGTTGTATGTGCAATGAAATCTTTTGTATATGATGATTA 1200
Qy 1201 AATGCAAGATGATTTATCTTAACTTGTGCGCAATGAGCTTATCTGCTGAGTATGATCT 1260
Db 1201 AATGCAAGATGATTTATCTTAACTTGTGCGCAATGAGCTTATCTGCTGAGTATGATCT 1260
Qy 1261 GGTGAGAGAGATGAGATAGGACGCCCCCAATATATATATGAGAAAAA 1320
Db 1261 GGTGAGAGAGATGAGATAGGACGCCCCCAATATATATATGAGAAAAA 1320
```

```
Qy 1321 AAAA 1324
Db 1321 AAAA 1324

RESULT 5
US-10-154-884B-665
; Sequence 665, Application US/10154884B
; Publication No. US2004000561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 665
; LENGTH: 1324
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-154-884B-665

Query Match 100.0%; Score 1324; DB 16; Length 1324;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1324; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTGAGAGGCTCTGGCTCTTCTTTAGGGGCGCCGAGAGCGCCATGCGGAGTCCCG 60
Db 1 CTTGAGAGGCTCTGGCTCTTCTTTAGGGGCGCCGAGAGCGCCATGCGGAGTCCCG 60
Qy 61 ACACCTGGGAGGAGCAGTACCGACCCGAGACCGCTGTGGGCTTGGAGAGTTGCTG 120
Db 61 ACACCTGGGAGGAGCAGTACCGACCCGAGACCGCTGTGGGCTTGGAGAGTTGCTG 120
Qy 121 TATTTGACGAGAGCAGACAGCCTGTGCTTACCAATCGAGATTAAGATAGTTA 180
Db 121 TATTTGACGAGAGCAGACAGCCTGTGCTTACCAATCGAGATTAAGATAGTTA 180
Qy 181 CAGTTAGCGGAGTCTTGGCTGCGGAGAGACGTCGCTGGGAGGCTTATGACCCCAAC 240
Db 181 CAGTTAGCGGAGTCTTGGCTGCGGAGAGACGTCGCTGGGAGGCTTATGACCCCAAC 240
Qy 241 CAGATTAGGCCAAGCCTGCTGCTATCATGTGGAGCCTTACCTGATGAGATACGA 300
Db 241 CAGATTAGGCCAAGCCTGCTGCTATCATGTGGAGCCTTACCTGATGAGATACGA 300
```



Dp	425	TCGACCTGTGCGCAGATGACGTGATGATGTGTTGGACACACCTGTCTCTTCAACCCA	481
Oy	428	GGGCTGAGCCTGGCCAGCCTTACAAATGGGAGATGTGTCTTCTTCACTTCCTGTACT	487
Dp	485	GGGCTGAGCCTGGCCAGCCTTACAAATGGGAGATGTGTGTCTTCTTCACTTCCTGTACT	544
Oy	488	ATGCTGTGTCTTCTTCCACACGCTGGGGGTCTGGGAGGAAATGACACAGAGAGATGAC	547
Dp	545	ATGCTGTGTCTTCTTCCACACGCTGGGGGTCTGGGAGGAAATGACACAGAGAGATGAC	604
Oy	548	TCTACCCAGGAGCCTGACAGACCTGCGCTTAGGCCACTCGCTCGCTTGTAGACTACACT	607
Dp	605	TCTACCCAGGAGCCTGACAGACCTGCGCTTAGGCCACTCGCTCGCTTGTAGACTACACT	664
Oy	608	CCTGCCAAGAGAGATTCCATTTGGCAGAGCTTCTTCCA-GGTGCCAGCTATACCTGTGC	666
Dp	665	CCTGCCAAGAGAGATTCCATTTGGCAGAGCTTCTTCCAAGGTGGCCAGCTATACCTGTGC	724
Oy	667	CTCGGCTTTTCTCACTGATGATAGTGTCTTCAAGCCTCTTTCGTCCCTTCTGTCCCTCAC	726
Dp	725	CTCGGCTTTTCTCACTGATGATAGTGTCTTCAAGCCTCTTTCGTCCCTTCTGTCCCTCAC	784
Oy	727	AGACTAGATTTCAATGTTGCACACCACTCAGCTCCCGTGAACCTTGAGAACACAGCGG	786
Dp	785	AGACTAGATTTCAATGTTGCACACCACTCAGCTCCCGTGAACCTTGAGAACACAGCGG	844
Oy	787	ATTCACTGAGCAGACCTCTGTAACCCCTGGAACAGATGCTTCACATGTGTGACGCTCG	846
Dp	845	ATTCACTGAGCAGACCTCTGTAACCCCTGGAACAGATGCTTCACATGTGTGACGCTCG	904
Oy	847	CATGTAAACAGCCTTGCAAAAGCCTGTGCCTGGTAAACAGCCTTGCAAGCGTGCCTGC	906
Dp	905	CATGTAAACAGCCTTGCAAAAGCCTGTGCCTGGTAAACAGCCTTGCAAGCGTGCCTGC	964
Oy	907	CGTAAACAGCCTTGCAAAAGCCTGTGCCTGGTAAACAGCCTTGCAAGCGTGCCTGC	966
Dp	965	CGTAAACAGCCTTGCAAAAGCCTGTGCCTGGTAAACAGCCTTGCAAGCGTGCCTGC	1022
Oy	967	CCTGAAGAGAGCCTTATCTGTGCTCAGGACTCAGAAAGCCTCTGGGTGAGTGTCCACT	1022
Dp	1025	CCTGAAGAGAGCCTTATCTGTGCTCAGGACTCAGAAAGCCTCTGGGTGAGTGTCCACT	1082
Oy	1027	CCCGGAGCGCAGCAGAGAGCCACAGCCGCGAGCCTGTGATGAGCCTCAGAACCTTGG	1088
Dp	1085	CCCGGAGCGCAGCAGAGAGCCACAGCCGCGAGCCTGTGATGAGCCTCAGAACCTTGG	1144
Oy	1087	GCTTGCCACGTGAAAAAGGATAGAGTGTGGGTTCCTCCCC-TTTATAGATGTGCACGC	1144
Dp	1145	GCTTGCCACGTGAAAAAGGATAGAGTGTGGGTTCCTCCCTTTTATAGATGTGCACGC	1200
Oy	1146	ACCTGGAGTGTACAAAGTTGTATGTGGCATGAATCTTTTGTATAGATGTGATTAATGC	1200
Dp	1205	ACCTGGAGTGTACAAAGTTGTATGTGGCATGAATCTTTTGTATAGATGTGATTAATGC	1266
Oy	1206	AAGATAGTTTATCTAACTTGTGCGCAATCAGCTTCTATCTTGAATTGATTTGTGTGG	1266
Dp	1265	AAGATAGTTTATCTAACTTGTGCGCAATCAGCTTCTATCTTGAATTGATTTGTGTGG	1322
Oy	1266	AGAGAACTGAGAAATGGCAGCCCCCAATTAATAATTTTCATGG 1309	
Dp	1325	AGAGAACTGAGAAATGGCAGCCCCCAATTAATAATTTTCATGG 1368	

RESULT 7  
US-10-117-722-871

```

; Sequence 877, Application US/10117722
; Publication No. US20030219744A1
;
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Drmanac, Radoje T.

```

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? TITLE OF INVENTION: No. US20030219744A1el Nucleic Acids and
? title OF INVENTION: Polypeptides
? FILE REFERENCE: 784CIP28CIP
? CURRENT FILING DATE: 2002-04-04
? PRIOR APPLICATION NUMBER: 09/620,312
? PRIOR FILING DATE: 2000-07-19
? PRIOR APPLICATION NUMBER: 09/552,317
? PRIOR FILING DATE: 2000-04-25
? PRIOR APPLICATION NUMBER: 09/488,725
? PRIOR FILING DATE: 2000-01-21
? NUMBER OF SEQ ID NOS: 1104
? SOFTWARE: pc_Fl_genes Version 1.0
? SEQ ID NO 871
? LENGTH: 1368
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (103)..(447)
? US-10-117-722-871

```

Query Match	96.7%	Score 1280;	DB 16;	Length 1368;
Best Local Similarity	99.8%;	Pred. No. 0;		
Matches 1302; Conservative	0;	Mismatches 0;	Indels 2;	Gaps 2

OY	8	GGCTCTGGCTCTTGTCTTTAGAGGGGCCCGAGAGACGCATGGCCAGTGGCCGACATCG	67
Db	65	GGCTCTGGCTCTTGTCTTTAGAGGGGCCCGAGAGACGCATGGCCAGTGGCCGACATCG	124
OY	68	GGAGAGCAGTCACCGACCACCCGGACCGCTGTGGGCTGTGGAGAGTTCGTATTTGG	127
Db	125	GGAGAGCAGTCACCGACCACCCGGACCGCTGTGGGCTGTGGAGAGTTCGTATTTGG	184
OY	128	ACGAGAGCAGCAGCGCTGGCTGGCCCTTAACATTCAGATTAAGATAGTTCAGTTAC	187
Db	185	ACGAGAGCAGCAGCGCTGGCTGGCCCTTAACATTCAGATTAAGATAGTTCAGTTAC	244
OY	188	GGGTGCTCTTGGCTCGGGAGACGTCGTCTGTGGGAGGCTTATGACCCCAACCCAGATAG	247
Db	245	GGGTGCTCTTGGCTCGGGAGACGTCGTCTGTGGGAGGCTTATGACCCCAACCCAGATAG	304
OY	248	GCCCAAGCTGCTGCTGCTTATCATATGTGGCAGCTCTACCTCGATGACAGATACCGATCTCTAG	307
Db	305	GCCCAAGCTGCTGCTGCTTATCATATGTGGCAGCTCTACCTCGATGACAGATACCGATCTCTAG	364
OY	308	ACTCCAGTTTGTGGCGCTTAGTGTATACCAACATCAAGATTGACGGCGTGAAGACATGCTTC	367
Db	365	ACTCCAGTTTGTGGCGCTTAGTGTATACCAACATCAAGATTGACGGCGTGAAGACATGCTTC	424
OY	368	TCGAGCTGCTGCCAGATGATGATATGTATGTCCTTGGCAGACCTGTCTCCTTTCACCCCA	427
Db	425	TCGAGCTGCTGCCAGATGATGATATGTATGTCCTTGGCAGACCTGTCTCCTTTCACCCCA	484
OY	428	GGGCTAGAGCCTGGCCACGACCTTACAAATGGGAGATGTGTGTTCTGTTCACCTTCGTTACT	487
Db	485	GGGCTAGAGCCTGGCCACGACCTTACAAATGGGAGATGTGTGTTCTGTTCACCTTCGTTACT	544
OY	488	ATGCTCTGTCTTCTCCACACGCTGTGGGCTGTGGAGAGATGACACAGAGATGAGC	547
Db	545	ATGCTCTGTCTTCTCCACACGCTGTGGGCTGTGGAGAGATGACACAGAGATGAGC	604
OY	548	TCCTACCAAGGCGCTGACAGACCTGCGCTGTAGCCACTCTGTGCTTATAGACATACCACT	607
Db	605	TCCTACCAAGGCGCTGACAGACCTCTGTACCCACTCTGTGCTTATAGACATACCACT	664
OY	608	CTTCCCAAGAGATTCATTTGGCAGAGCTTCTTCCA-GGTGCCAGACTATACCTGTGC	666
Db	665	CTTCCCAAGAGATTCATTTGGCAGAGCTTCTTCCAAGGTTGCCAGACTATACCTGTGC	724
OY	667	CTGGGCTTTTCTCAGCTGAGATGATGTGTCCTTATGCTCTTCTGTCTGTCCCTAC	726
Db	725	CTGGGCTTTTCTCAGCTGAGATGATGTGTCCTTATGCTCTTCTGTCTGTCCCTAC	784

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Qy 727 AGACATGATATTTGATGTTGACACCCACTGAGCTCCGTAACCTTGAGAAACAGCCG 786
Dy 785 AGCACTAGTATTTATGTTGACACCCACTGAGCTCCGTAACCTTGAGAAACAGCCG 844
Qy 787 ATTCACCTGACGAGACCTCTGAAACCTTGACAGTGTCTCATATGTTGCTACGCGCTG 846
Dy 845 ATTCACCTGACGAGACCTCTGAAACCTTGACAGTGTCTCATATGTTGCTACGCGCTG 904
Qy 847 CATGTAAACAGCCTTGCAAAAGCTGCTGCGGTAAACAGCCTTGCAAAAGCCTGCTGCC 906
Dy 905 CATGTAAACAGCCTTGCAAAAGCTGCTGCGGTAAACAGCCTTGCAAAAGCCTGCTGCC 964
Qy 907 CGTAAACAGCCTTGCAAAAGCTGCTGCGGTAAACAGCCTTGCAAAAGCCTGCTGCC 966
Dy 965 CGTAAACAGCCTTGCAAAAGCTGCTGCGGTAAACAGCCTTGCAAAAGCCTGCTGCC 1024
Qy 967 CCGTAAAGAGACCTTATCTGTGCTCAGAGCTCAGAAAGCCTGCGGTCAAGTGTCAAT 1026
Dy 1025 CCGTAAAGAGACCTTATCTGTGCTCAGAGCTCAGAAAGCCTGCGGTCAAGTGTCAAT 1084
Qy 1027 CCGCGGAGCGCAGAGAGGCCAGGCGCGGAGCCCTGTGATGAGCCCTCAGAAAGCCTTG 1086
Dy 1085 CCGCGGAGCGCAGAGAGGCCAGGCGCGGAGCCCTGTGATGAGCCCTCAGAAAGCCTTG 1144
Qy 1087 GCTTGCCCAAGTGAAGGATGAGGTTGGGTTTCCCGCC-TTTATAGATGGTCAAGC 1145
Dy 1145 GCTTGCCCAAGTGAAGGATGAGGTTGGGTTTCCCGCCCTTTATAGATGGTCAAGC 1204
Qy 1146 ACCTGGGTGTTCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1205
Dy 1205 ACCTGGGTGTTCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1264
Qy 1206 AAGATAGTTATCTTAATCTTGCGGCAATCAGCTTTCTTATCTTGATGATGATGATGATG 1265
Dy 1265 AAGATAGTTATCTTAATCTTGCGGCAATCAGCTTTCTTATCTTGATGATGATGATGATG 1324
Qy 1266 AGAAGAGTGAATAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1309
Dy 1325 AGAAGAGTGAATAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1368

RESULT 8
US-10-057-475B-10484
; Sequence 10484, Application US/10057475B
; Publication No. US20040002068A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aljun
; APPLICANT: Ordenez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-014402US
; CURRENT FILING DATE: US/10/057, 475B
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
```

```
;; PRIOR APPLICATION NUMBER: US 60/202,084
;; PRIOR FILING DATE: 2000-05-04
;; PRIOR APPLICATION NUMBER: US 60/206,201
;; PRIOR FILING DATE: 2000-05-22
;; PRIOR APPLICATION NUMBER: US 60/218,950
;; PRIOR FILING DATE: 2000-07-14
;; PRIOR APPLICATION NUMBER: US 60/222,903
;; PRIOR FILING DATE: 2000-08-03
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 10979
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 10484
;; LENGTH: 369
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: His-TCL-1, TCL-1 with His tag
US-10-057-475B-10484
Query Match 26.0%; Score 344; DB 16; Length 369;
Best Local Similarity 100.0%; Pred. No. 1.6e-100;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 49 GCCGAGTGCCTGACACTCGGAGAGGAGTCAAGCACCAGCCGCTGTGGCCTTG 108
Dy 25 GCCGAGTGCCTGACACTCGGAGAGGAGTCAAGCACCAGCCGCTGTGGCCTTG 84
Qy 109 GAGAACTGCTGTATTTTGGACGAGAAACAGCAGCCTGCTGCTTAAACATCGAGATA 168
Dy 85 GAGAACTGCTGTATTTTGGACGAGAAACAGCAGCCTGCTGCTTAAACATCGAGATA 144
Qy 169 AAGATAGTTAAGTTCAGGAGTGTCTTGTGCGGAGACGTCGCTGAGGAGGCT 228
Dy 145 AAGATAGTTAAGTTCAGGAGTGTCTTGTGCGGAGACGTCGCTGAGGAGGCT 204
Qy 229 ATGACCCCAACCAAGATGAGGCCAAGCTGCTGCTTATCATGTGGAGCTCTACCTGAT 288
Dy 205 ATGACCCCAACCAAGATGAGGCCAAGCTGCTGCTTATCATGTGGAGCTCTACCTGAT 264
Qy 289 GAGCAGTACCGATCTTCAGACTCAGCTTCTGCGGCTTATGATGATGATGATGATGATGATG 348
Dy 265 GAGCAGTACCGATCTTCAGACTCAGCTTCTGCGGCTTATGATGATGATGATGATGATGATG 324
Qy 349 GCGGTGAGGAGCATGCTTCTCGAGCTGCTGCCAGATGACTGATG 392
Dy 325 GCGGTGAGGAGCATGCTTCTCGAGCTGCTGCCAGATGACTGATG 368

RESULT 9
US-10-154-884B-10484
; Sequence 10484, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013521US
; CURRENT FILING DATE: US/10/154, 884B
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-04-28
```

;; PRIOR APPLICATION NUMBER: US 60/200,999  
;; PRIOR FILING DATE: 2000-05-01  
;; PRIOR APPLICATION NUMBER: US 60/202,084  
;; PRIOR FILING DATE: 2000-05-04  
;; PRIOR APPLICATION NUMBER: US 60/206,201  
;; PRIOR FILING DATE: 2000-05-22  
;; PRIOR APPLICATION NUMBER: US 60/218,950  
;; PRIOR FILING DATE: 2000-07-14  
;; PRIOR APPLICATION NUMBER: US 60/222,903  
;; PRIOR FILING DATE: 2000-08-03  
;; Remaining Prior Application data removed - See File Wrapper or PALM.  
;; NUMBER OF SEQ ID NOS: 11290  
;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO 10484  
;; LENGTH: 369  
;; TYPE: DNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: His-TCL-1, TCL-1 with His tag  
US-10-154-884B-10484

Query Match 26.0%; Score 344; DB 16; Length 369;

Best Local Similarity 100.0%; Pred. No. 1,6e-100; Indels 0; Gaps 0;

Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 49 GCCGAGTCCCGACACTCGGGAGGAGGAGTCAACCGACCGCGGAGCGCTGTGGGCTGG 108  
Db 25 GCCGAGTCCCGACACTCGGGAGGAGGAGTCAACCGACCGCGGAGCGCTGTGGGCTGG 84  
Qy 109 GAGAAATTGCTATTTGAGACGAGAGACAGCGCTGCGCTTAAACATCGAGATA 168  
Db 85 GAGAAATTGCTATTTGAGACGAGAGACAGCGCTGCGCTTAAACATCGAGATA 144  
Qy 169 AAGATAGATTACATTACGGGTGCTTTGGCTCGGGAAAGAGTGTCTGGGGAGGCTT 228  
Db 145 AAGATAGATTACATTACGGGTGCTTTGGCTCGGGAAAGAGTGTCTGGGGAGGCTT 204  
Qy 229 ATGACCCCGACCGATAGGCGGACCGTGCCTTATCATGTGAGCAGTCAACCTGAT 288  
Db 205 ATGACCCCGACCGATAGGCGGACCGTGCCTTATCATGTGAGCAGTCAACCTGAT 264  
Qy 289 GAGCAGATCCGATCTCCAGACTCCAGTTTCTGGCGCTTAGTATACATCAAGATTGAC 348  
Db 265 GAGCAGATCCGATCTCCAGACTCCAGTTTCTGGCGCTTAGTATACATCAAGATTGAC 324  
Qy 349 GCGGTGAGAGACATGCTTCTCGAGCTGCTGCCAGATGACTGATG 392  
Db 325 GCGGTGAGAGACATGCTTCTCGAGCTGCTGCCAGATGACTGATG 368

## RESULT 10

US-09-796-692-321/c  
;; Sequence 321, Application US/09796692  
;; Publication No. US20020198362a1  
;; GENERAL INFORMATION:  
;; APPLICANT: Gaiger, Alexander  
;; APPLICANT: Algate, Paul A.  
;; APPLICANT: Mannion, Jane  
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY  
;; FILE REFERENCE: 2077, 001200  
;; CURRENT APPLICATION NUMBER: US/09/796,692  
;; PRIOR APPLICATION NUMBER: 60/186,126  
;; PRIOR FILING DATE: 2000-03-01  
;; PRIOR APPLICATION NUMBER: 60/190,479  
;; PRIOR FILING DATE: 2000-03-17  
;; PRIOR APPLICATION NUMBER: 60/200,545  
;; PRIOR FILING DATE: 2000-04-27  
;; PRIOR APPLICATION NUMBER: 60/200,303  
;; PRIOR FILING DATE: 2000-04-28  
;; PRIOR APPLICATION NUMBER: 60/200,779  
;; PRIOR FILING DATE: 2000-04-28

;; PRIOR APPLICATION NUMBER: 60/200,999  
;; PRIOR FILING DATE: 2000-05-01  
;; PRIOR APPLICATION NUMBER: 60/202,084  
;; PRIOR FILING DATE: 2000-05-04  
;; PRIOR APPLICATION NUMBER: 60/206,201  
;; PRIOR FILING DATE: 2000-05-22  
;; PRIOR APPLICATION NUMBER: 60/218,950  
;; PRIOR FILING DATE: 2000-07-14  
;; PRIOR APPLICATION NUMBER: 60/222,903  
;; PRIOR FILING DATE: 2000-08-03  
;; PRIOR APPLICATION NUMBER: 60/223,416  
;; PRIOR FILING DATE: 2000-08-04  
;; PRIOR APPLICATION NUMBER: 60/223,378  
;; PRIOR FILING DATE: 2000-08-07  
;; NUMBER OF SEQ ID NOS: 9597  
;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO 321  
;; LENGTH: 285  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-09-796-692-321

Query Match 21.5%; Score 285; DB 9; Length 285;

Best Local Similarity 100.0%; Pred. No. 1,9e-81; Indels 0; Gaps 0;

Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 682 CTGATGATGCTTTACAGCTCTTTCTCTCCCTTTGTGCTCCTACAGCACTAGTATTTCA 741  
Db 285 CTGATGATGCTTTACAGCTCTTTCTCTCCCTTTGTGCTCCTACAGCACTAGTATTTCA 226  
Qy 742 TGTTCACACCCACTCAGCTCCGTGAACCTGTGAGAACACAGCCGATTCACCTGACAGG 801  
Db 225 TGTTCACACCCACTCAGCTCCGTGAACCTGTGAGAACACAGCCGATTCACCTGACAGG 166  
Qy 802 ACTCTGAACCTTGACAGATGCTTCACATGTGTACATGCTGATGATTAACAGCGCT 861  
Db 165 ACTCTGAACCTTGACAGATGCTTCACATGTGTACATGCTGATGATTAACAGCGCT 106  
Qy 862 GCAAAAGCTGCTGCGGTAAACACAGCTGCTGCAAAAGCTGCTGCTGCTGCTGCTGCTG 921  
Db 105 GCAAAAGCTGCTGCGGTAAACACAGCTGCTGCAAAAGCTGCTGCTGCTGCTGCTGCTG 46  
Qy 922 AAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 966  
Db 45 AAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1

## RESULT 11

US-09-796-692-468/c  
;; Sequence 468, Application US/09796692  
;; Publication No. US20020198362a1  
;; GENERAL INFORMATION:  
;; APPLICANT: Gaiger, Alexander  
;; APPLICANT: Algate, Paul A.  
;; APPLICANT: Mannion, Jane  
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY  
;; FILE REFERENCE: 2077, 001200  
;; CURRENT APPLICATION NUMBER: US/09/796,692  
;; PRIOR APPLICATION NUMBER: 60/186,126  
;; PRIOR FILING DATE: 2000-03-01  
;; PRIOR APPLICATION NUMBER: 60/190,479  
;; PRIOR FILING DATE: 2000-03-17  
;; PRIOR APPLICATION NUMBER: 60/200,545  
;; PRIOR FILING DATE: 2000-04-27  
;; PRIOR APPLICATION NUMBER: 60/200,303  
;; PRIOR FILING DATE: 2000-04-28  
;; PRIOR APPLICATION NUMBER: 60/200,779  
;; PRIOR FILING DATE: 2000-04-28  
;; PRIOR APPLICATION NUMBER: 60/200,999  
;; PRIOR FILING DATE: 2000-05-01  
;; PRIOR APPLICATION NUMBER: 60/202,084

;; PRIOR FILING DATE: 2000-05-04  
;; PRIOR APPLICATION NUMBER: 60/206,201  
;; PRIOR FILING DATE: 2000-05-22  
;; PRIOR APPLICATION NUMBER: 60/218,950  
;; PRIOR FILING DATE: 2000-07-14  
;; PRIOR APPLICATION NUMBER: 60/222,903  
;; PRIOR FILING DATE: 2000-08-03  
;; PRIOR APPLICATION NUMBER: 60/223,416  
;; PRIOR FILING DATE: 2000-08-04  
;; PRIOR APPLICATION NUMBER: 60/223,378  
;; PRIOR FILING DATE: 2000-08-07  
;; NUMBER OF SEQ ID NOS: 9597  
;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO 468  
;; LENGTH: 285  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-09-796-692-468

Query Match 21.5%; Score 285; DB 9; Length 285;  
Best Local Similarity 100.0%; Pred. No. 1,9e-81;  
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 682 CTGATGATGATGCTTCAGCCCTCTTCTGTCCTCTGCTCCTCAGACAGACTAGATTTC 741  
DB 285 CTGATGATGATGCTTCAGCCCTCTTCTGTCCTCTGCTCCTCAGACAGACTAGATTTC 226  
QY 742 TGTTCACACCCACTCAGCTCCGTGAACCTTGAGAACACAGCCGATTCACTGAGCAG 801  
DB 225 TGTTCACACCCACTCAGCTCCGTGAACCTTGAGAACACAGCCGATTCACTGAGCAG 166  
QY 802 ACCCTGAAACCTCGACCAATGCTTCACATGCTGTACAGCCCGCATGTAACAGCCCT 861  
DB 165 ACCCTGAAACCTCGACCAATGCTTCACATGCTGTACAGCCCGCATGTAACAGCCCT 106  
QY 862 GCAACGCTGCTGCGGTAAACAGCGCTGCAACAGCTGCTGCGGTAAACAGCGCTGC 921  
DB 105 GCAACGCTGCTGCGGTAAACAGCGCTGCAACAGCTGCTGCGGTAAACAGCGCTGC 46  
QY 922 AAACGCTGCTGCGGTAAACAGCGCTGCAACAGCTGCTGCGGTAAACAGCGCTGC 966  
DB 45 AAACGCTGCTGCGGTAAACAGCGCTGCAACAGCTGCTGCGGTAAACAGCGCTGC 1

RESULT 12  
US-09-796-692-3032  
;; Sequence 3032, Application US/09796692  
;; Publication No. US20020198362A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Gaiger, Alexander  
;; APPLICANT: Algate, Paul A.  
;; APPLICANT: Mannion, Jane  
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY  
;; FILE REFERENCE: 2077.001200  
;; CURRENT APPLICATION NUMBER: US/09/796,692  
;; CURRENT FILING DATE: 2001-03-01  
;; PRIOR APPLICATION NUMBER: 60/186,126  
;; PRIOR FILING DATE: 2000-03-01  
;; PRIOR APPLICATION NUMBER: 60/190,479  
;; PRIOR FILING DATE: 2000-03-17  
;; PRIOR APPLICATION NUMBER: 60/200,545  
;; PRIOR FILING DATE: 2000-04-27  
;; PRIOR APPLICATION NUMBER: 60/200,303  
;; PRIOR FILING DATE: 2000-04-28  
;; PRIOR APPLICATION NUMBER: 60/200,779  
;; PRIOR FILING DATE: 2000-04-28  
;; PRIOR APPLICATION NUMBER: 60/200,999  
;; PRIOR FILING DATE: 2000-05-01  
;; PRIOR APPLICATION NUMBER: 60/202,084  
;; PRIOR FILING DATE: 2000-05-04  
;; PRIOR APPLICATION NUMBER: 60/206,201  
;; PRIOR FILING DATE: 2000-05-22

;; PRIOR APPLICATION NUMBER: 60/218,950  
;; PRIOR FILING DATE: 2000-07-14  
;; PRIOR APPLICATION NUMBER: 60/222,903  
;; PRIOR FILING DATE: 2000-08-03  
;; PRIOR APPLICATION NUMBER: 60/223,416  
;; PRIOR FILING DATE: 2000-08-04  
;; PRIOR APPLICATION NUMBER: 60/223,378  
;; PRIOR FILING DATE: 2000-08-07  
;; NUMBER OF SEQ ID NOS: 9597  
;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO 3032  
;; LENGTH: 285  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-09-796-692-3032

Query Match 21.5%; Score 285; DB 9; Length 285;  
Best Local Similarity 100.0%; Pred. No. 1,9e-81;  
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 682 CTGATGATGATGCTTCAGCCCTCTTCTGTCCTCTGCTCCTCAGACAGACTAGATTTC 741  
DB 1 CTGATGATGATGCTTCAGCCCTCTTCTGTCCTCTGCTCCTCAGACAGACTAGATTTC 60  
QY 742 TGTTCACACCCACTCAGCTCCGTGAACCTTGAGAACACAGCCGATTCACTGAGCAG 801  
DB 61 TGTTCACACCCACTCAGCTCCGTGAACCTTGAGAACACAGCCGATTCACTGAGCAG 120  
QY 802 ACCCTGAAACCTCGACCAATGCTTCACATGCTGTACAGCCCGCATGTAACAGCCCT 861  
DB 121 ACCCTGAAACCTCGACCAATGCTTCACATGCTGTACAGCCCGCATGTAACAGCCCT 180  
QY 862 GCAACGCTGCTGCGGTAAACAGCGCTGCAACAGCTGCTGCGGTAAACAGCGCTGC 921  
DB 181 GCAACGCTGCTGCGGTAAACAGCGCTGCAACAGCTGCTGCGGTAAACAGCGCTGC 240  
QY 922 AAACGCTGCTGCGGTAAACAGCGCTGCAACAGCTGCTGCGGTAAACAGCGCTGC 966  
DB 241 AAACGCTGCTGCGGTAAACAGCGCTGCAACAGCTGCTGCGGTAAACAGCGCTGC 285

RESULT 13  
US-09-796-692-5832/c  
;; Sequence 5832, Application US/09796692  
;; Publication No. US20020198362A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Gaiger, Alexander  
;; APPLICANT: Algate, Paul A.  
;; APPLICANT: Mannion, Jane  
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY  
;; FILE REFERENCE: 2077.001200  
;; CURRENT APPLICATION NUMBER: US/09/796,692  
;; CURRENT FILING DATE: 2001-03-01  
;; PRIOR APPLICATION NUMBER: 60/186,126  
;; PRIOR FILING DATE: 2000-03-01  
;; PRIOR APPLICATION NUMBER: 60/190,479  
;; PRIOR FILING DATE: 2000-03-17  
;; PRIOR APPLICATION NUMBER: 60/200,545  
;; PRIOR FILING DATE: 2000-04-27  
;; PRIOR APPLICATION NUMBER: 60/200,303  
;; PRIOR FILING DATE: 2000-04-28  
;; PRIOR APPLICATION NUMBER: 60/200,779  
;; PRIOR FILING DATE: 2000-04-28  
;; PRIOR APPLICATION NUMBER: 60/200,999  
;; PRIOR FILING DATE: 2000-05-01  
;; PRIOR APPLICATION NUMBER: 60/202,084  
;; PRIOR FILING DATE: 2000-05-04  
;; PRIOR APPLICATION NUMBER: 60/206,201  
;; PRIOR FILING DATE: 2000-05-22  
;; PRIOR APPLICATION NUMBER: 60/218,950  
;; PRIOR FILING DATE: 2000-07-14  
;; PRIOR APPLICATION NUMBER: 60/222,903

;; PRIOR FILING DATE: 2000-08-03  
;; PRIOR APPLICATION NUMBER: 60/223,416  
;; PRIOR FILING DATE: 2000-08-04  
;; PRIOR APPLICATION NUMBER: 60/223,378  
;; PRIOR FILING DATE: 2000-08-07  
;; NUMBER OF SEQ ID NOS: 9597  
;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO: 5832  
;; LENGTH: 285  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-09-796-692-5832

Query Match 21.5%; Score 285; DB 9; Length 285;  
Best Local Similarity 100.0%; Pred. No. 1.9e-81;  
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 682 CTGATGATGGTCTTCAAGCCTCTTCTGTCCTCTGTCCTCAGACAGACTAGTATTTCA 741  
DB 285 CTGATGATGGTCTTCAAGCCTCTTCTGTCCTCTGTCCTCAGACAGACTAGTATTTCA 226  
QY 742 TGTTCACACCCACTCAGCTCCGTGAACCTTGTGAACAACAGCCGATTCACTGACAG 801  
DB 225 TGTTCACACCCACTCAGCTCCGTGAACCTTGTGAACAACAGCCGATTCACTGACAG 166  
QY 802 ACCTTGAACCCCTGACAGTGTCTCAATGAGTCAAGCCTGACATGTAACAGCGCT 861  
DB 165 ACCTTGAACCCCTGACAGTGTCTCAATGAGTCAAGCCTGACATGTAACAGCGCT 106  
QY 862 GCAACGCTGCTGCGGTAAACAGCCTGCAACGCTGCTGCCCTGTAACACCGCTGC 921  
DB 105 GCAACGCTGCTGCGGTAAACAGCCTGCAACGCTGCTGCCCTGTAACACCGCTGC 46  
QY 922 AAACGCTGCTGCCACACAGTTACGTCGACGCTCAAGAAAG 966  
DB 45 AAACGCTGCTGCCACACAGTTACGTCGACGCTCAAGAAAG 1

## RESULT 14

US-09-796-692-6894/c  
;; Sequence 6894, Application US/09796692  
;; Publication No. US20020198362A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Gaiger, Alexander  
;; APPLICANT: Algate, Paul A.  
;; APPLICANT: Mannion, Jane  
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY  
;; FILE REFERENCE: 2077.001200  
;; CURRENT APPLICATION NUMBER: US/09/796,692  
;; PRIOR FILING DATE: 2001-03-01  
;; PRIOR APPLICATION NUMBER: 60/186,126  
;; PRIOR FILING DATE: 2000-03-01  
;; PRIOR APPLICATION NUMBER: 60/190,479  
;; PRIOR FILING DATE: 2000-03-17  
;; PRIOR APPLICATION NUMBER: 60/200,545  
;; PRIOR FILING DATE: 2000-04-27  
;; PRIOR APPLICATION NUMBER: 60/200,303  
;; PRIOR FILING DATE: 2000-04-28  
;; PRIOR APPLICATION NUMBER: 60/200,779  
;; PRIOR FILING DATE: 2000-04-28  
;; PRIOR APPLICATION NUMBER: 60/200,999  
;; PRIOR FILING DATE: 2000-05-01  
;; PRIOR APPLICATION NUMBER: 60/202,084  
;; PRIOR FILING DATE: 2000-05-04  
;; PRIOR APPLICATION NUMBER: 60/206,201  
;; PRIOR FILING DATE: 2000-05-22  
;; PRIOR APPLICATION NUMBER: 60/218,950  
;; PRIOR FILING DATE: 2000-07-14  
;; PRIOR APPLICATION NUMBER: 60/222,903  
;; PRIOR FILING DATE: 2000-08-03  
;; PRIOR APPLICATION NUMBER: 60/223,416  
;; PRIOR FILING DATE: 2000-08-04

;; PRIOR APPLICATION NUMBER: 60/223,378  
;; PRIOR FILING DATE: 2000-08-07  
;; NUMBER OF SEQ ID NOS: 9597  
;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO: 6894  
;; LENGTH: 285  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-09-796-692-6894

Query Match 21.5%; Score 285; DB 9; Length 285;  
Best Local Similarity 100.0%; Pred. No. 1.9e-81;  
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 682 CTGATGATGGTCTTCAAGCCTCTTCTGTCCTCTGTCCTCAGACAGACTAGTATTTCA 741  
DB 285 CTGATGATGGTCTTCAAGCCTCTTCTGTCCTCTGTCCTCAGACAGACTAGTATTTCA 226  
QY 742 TGTTCACACCCACTCAGCTCCGTGAACCTTGTGAACAACAGCCGATTCACTGACAG 801  
DB 225 TGTTCACACCCACTCAGCTCCGTGAACCTTGTGAACAACAGCCGATTCACTGACAG 166  
QY 802 ACCTTGAACCCCTGACAGTGTCTCAATGAGTCAAGCCTGACATGTAACAGCGCT 861  
DB 165 ACCTTGAACCCCTGACAGTGTCTCAATGAGTCAAGCCTGACATGTAACAGCGCT 106  
QY 862 GCAACGCTGCTGCGGTAAACAGCCTGCAACGCTGCTGCCCTGTAACACCGCTGC 921  
DB 105 GCAACGCTGCTGCGGTAAACAGCCTGCAACGCTGCTGCCCTGTAACACCGCTGC 46  
QY 922 AAACGCTGCTGCCACACAGTTACGTCGACGCTCAAGAAAG 966  
DB 45 AAACGCTGCTGCCACACAGTTACGTCGACGCTCAAGAAAG 1

## RESULT 15

US-10-040-862-321/c  
;; Sequence 321, Application US/10040862  
;; Publication No. US20030078396A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Gaiger, Alexander  
;; APPLICANT: Algate, Paul A.  
;; APPLICANT: Mannion, Jane  
;; APPLICANT: Retter, Marc  
;; APPLICANT: Corixa Corporation  
;; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy  
;; FILE REFERENCE: 014058-013520US  
;; CURRENT APPLICATION NUMBER: US/10/040,862  
;; PRIOR FILING DATE: 2001-11-06  
;; PRIOR APPLICATION NUMBER: US 60/186,126  
;; PRIOR FILING DATE: 2000-03-01  
;; PRIOR APPLICATION NUMBER: US 60/190,479  
;; PRIOR FILING DATE: 2000-03-17  
;; PRIOR APPLICATION NUMBER: US 60/200,545  
;; PRIOR FILING DATE: 2000-04-27  
;; PRIOR APPLICATION NUMBER: US 60/200,303  
;; PRIOR FILING DATE: 2000-04-28  
;; PRIOR APPLICATION NUMBER: US 60/200,779  
;; PRIOR FILING DATE: 2000-04-28  
;; PRIOR APPLICATION NUMBER: US 60/200,999  
;; PRIOR FILING DATE: 2000-05-01  
;; PRIOR APPLICATION NUMBER: US 60/202,084  
;; PRIOR FILING DATE: 2000-05-04  
;; PRIOR APPLICATION NUMBER: US 60/206,201  
;; PRIOR FILING DATE: 2000-05-22  
;; PRIOR APPLICATION NUMBER: US 60/218,950  
;; PRIOR FILING DATE: 2000-07-14  
;; PRIOR APPLICATION NUMBER: US 60/222,903  
;; PRIOR FILING DATE: 2000-08-03  
;; PRIOR APPLICATION NUMBER: US 60/223,416  
;; PRIOR FILING DATE: 2000-08-04  
;; PRIOR APPLICATION NUMBER: US 60/223,378

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; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 321
; LENGTH: 285
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-040-862-321

```

```

Query Match      21.5%; Score 285; DB 15; Length 285;
Best Local Similarity 100.0%; Pred. No. 1.9e-81;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 682 CTGATGATGATGCTTTCAGCCTCTTCTGTGTCCTCTGTCCTCAAGACTAGTATTCA 741
   |||||||
Db 285 CTGATGATGCTTTCAGCCTCTTCTGTGTCCTCTGTCCTCAAGACTAGTATTCA 226
   |||||||

QY 742 TGTGACACCCACTCAGCTCCGTGAACCTTGGAACACAGCCGATTCACTGAGCAGG 801
   |||||||
Db 225 TGTGACACCCACTCAGCTCCGTGAACCTTGGAACACAGCCGATTCACTGAGCAGG 166
   |||||||

QY 802 ACCTCTGAACCTTGGAACCTTGGAACCTTGGAACCTTGGAACCTTGGAACCTTGGA 861
   |||||||
Db 165 ACCTCTGAACCTTGGAACCTTGGAACCTTGGAACCTTGGAACCTTGGAACCTTGGA 106
   |||||||

QY 862 GCAAAACGCTGCTGCGGTAAACAGCGCTGCAACAGCGCTGCAACAGCGCTGCAACAG 921
   |||||||
Db 105 GCAAAACGCTGCTGCGGTAAACAGCGCTGCAACAGCGCTGCAACAGCGCTGCAACAG 46
   |||||||

QY 922 AAACGCTGCTGCGGTAAACAGCGCTGCAACAGCGCTGCAACAGCGCTGCAACAG 966
   |||||||
Db 45 AAACGCTGCTGCGGTAAACAGCGCTGCAACAGCGCTGCAACAGCGCTGCAACAG 1
   |||||||

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Search completed: June 17, 2004, 14:25:05  
Job time : 618 secs